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OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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gb_ba3:*
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1	gb_htg9: * gb_htg10: * gb_htg11: * gb_htg11: * gb_htg13: * gb_htg13: * gb_htg15: * gb_htg15: * gb_htg15: * gb_htg15: * gb_htg15: * gb_htg15: * gb_htg16: * gb_htg16: * gb_htg17: * gb_htg18: * gb_htg18: * gb_htg18: * gb_htg21: * gb_htg22: * gb_htg2	ov:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

8	თ თ	4	w	2	ם	Result No.
191.8 191.8	194.4 191.8	194.8	207.2	1362		Score
14,1 14,1	14,3 14,1	14.3	15.2	100.0	100.0	Query Match Length
1317 2128	1206 1317	108873	3508	3435	1362	Query Match Length DB
88	94 10	5 80	94	89	10	) B
AF102542	AB037597 AX087948	AF318573	AB037596	AF132035	AX087935	ID
AF038650 Homo sapi AF102542 Homo sapi	AB037597 Mus muscu AX087948 Sequence	AF318573 Bovine he	AB037596 Mus muscu	AF132035 Homo sapi	AX087935 Sequence	Description

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1 (bases 1 to 1562)
Schwientek, T. and Clausen, H.

Udp-n-acetylglucosamine: galactose-_g(b)1,3- n
-acetylglucosamine-_g(a)-r/(glonac to galnac) _g(b)1,6- n
-acetylglucosamine-g(a)-r/(glonac to galnac) _g(b)1,6- n
-acetylglucosaminyltransferas e, c2gnt3
-patent: WO 0114535-A 1 01-MAR-2001;
Schwientek, Tilo (DK); Clausen, Henrik (DK)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX087935 1362 bp DNA
Sequence 1 from Patent WOO114535.
AX087935
AX087935.1 GI:13396913
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CIHYDRKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSI
                                                                                                                                                                          /note="The gene of C2GnT3"
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AC022480 Homo sapi
AF231105 Bovine he
U68192 Mus musculu
AL139039 Human DNA
AL138077 Homo sapi
AC021626 Homo sapi
AX087950 Sequence
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219507 Sequence 13
219509 Human I bet
AC076970 Homo sapi
AL19659 Human I NA
AC021626 Homo sapi
AC073815 Mus muscu
AX045251 Sequence
AX045253 Sequence
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AX045253 Mus musculu
AL18757 Homo sapi
AL16626 Human DNA
379797 enzymatic g
L41605 Human beta-
D87332 Mus musculu
Z46386 Bovine herp
AX087946 Sequence 3
172548 Sequence 3
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QWKYVINLCGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLER EYYKLPIRTNISKEAPPHNIQIFVGSAFFVKJSAFVKJSAFVKJSAFVKJSAFVKJSAFVKJSAFVKJSAFVKJSAFVKJSAFVKJSAFVKJIFNNSIVO DEHFWATILRVPGIFGEIGSSAGOVSDLOSKTRLYKWNYYEGFFFF YGAAELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQQRDWITI TTS" 260 c 279 g 413 t  IGIN  100.0%; Score 1362; DB 10; Length 1362 Best Local Similarity 100.0%; Pred. No.'0; Best Local Similarity 100.0%; Pred. No.'0; Matches 1362; Conservative 0; Mismatches 0; Indels 0;  1 atgaagatattcaaatgttatttttaaacataccctacagcagaaagttttcatcctg [	HHEELRRVPY AMMONDTYSP GSHLRSVCI KLEMDRNLT KLEMDRNLT 120 120 120 120 120 120 120 120 120 120
 121 aaagacatttacttg	N N H H
QY 241 cctttggaaattggaaagagtctggaaataagaaggaacggacatcattgacttggaggat	300
1 caaaagettgtete             1 CAAAAGETTGTCTC	4 4 2
 Qy 421 aaagatgcaattattggttgaaaggcttatccatgctatatacaaccagcacaatatttac	480 480 540
Qy 541 aagtgcttctccaatattttcattgcttccaaatttagaggctgtggaatatgccacatt	5 6000
61 aaatatgttatcaacttgtgtgggcaagattttcccctgaagtcaaattttgaati 	72 72
 Qy 721 tcagagttgaaaaaactcaatggagcaaatatgttggagacggtgaaacccccaaacagt 	780
gggtgccttatgaatatgtgaa 	9 840 - 840 - 900
A 941 CLGCCGGTGGGGGGCGCCCCCGGGGGGGGCGCCCCCGGGGGG	

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Homo sapiens (C2GnT3) mRNA
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AF132035.1 G:
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Schwientek, T., Yeh, J.C., Levery, S.B., Keck, B., Merkx, G., van Kessel, A.G., Fukuda, M. and Clausen, H. Control of Orglycan branch formation. Molecular cloning and characterization of a novel thymus-associated core 2 betal, 6-n-acetylglucosaminyltransferase J. Biol. Chem. 275 (15), 11106-11113 (2000)
                                                                                                                                                    Direct Submission
Submitted (27-FEB-1999) School of Dentistry,
Copenhagen, Norre Alle 20, Copenhagen 2200,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       Homo
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ind Clausen,H.
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VVAMTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVYHKDAIMVERLIHAIYNOHNIY
CIHYDRKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSI
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YGAABATLIKVPGIPGEISRSAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCI
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TTS"

1032 a 678 c 651 g 1074 t
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BASE COUNT
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Eukaryota; Me
                                                                                                              Direct Submission
Submitted (25-JAN-2000) to the DDBJ/EMBL/GenBank databases.
Nobuyuki Kurosawa, Nagoya University School of Medicine, Departme of Biochemistry; 65 Tsurumai-cho, Showa-ku, Nagoya, Aichi 466-855 Japan (E-mail:nkuro@tsuru.med.nagoya-u.ac.jp, Tel:81-52-744-2063, Fax:81-52-744-2065)
                                                                                                                                                                                                                       A novel variant form of murine beta-1,
6-N-acetylglucosaminyltransferase forming
poly-N-acetyllactosamines
Glycobiology 10 (10), 1001-1011 (2000)
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      /db_xref="taxon:10090"
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tctcctgatgagcacttttgggctaccttgattcgggttccaggaatacctgggggagatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCACAACCTGACCATTTACTTTGGCACTGCTTATGTGGCTCTCACACGGGAATTTGCT
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                                                             tccagatcagcccaggatgtgtctgatctgcagagtaagactcgccttgtcaagtggaat
                                                                                                                                           AGTCCTGATGAGCACTTCTGGGTGACACTCAATAGGATCCCTGGAGTCCCTGGCTCCATG
                                                                                                                                                                                                                                                                                          AACTTTGTCCTCAAAGACCAGCGTTCAGTAGACTTAATCTCCTGGTCCAAGGACACGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgggtgccttatgaatatgtgaagctaccaataaggacaaacatctccaaggaagcaccc
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//codon_start=1
//codon_start=1
//product="beta-1,6-N-acetylglucosaminyltransferase B"
/protein_id="BAB03495.1"
//db_xref="G1:9650954"
//db_xref=
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Bovine herpesvirus 4 long unique region, complete sequence.
AF318573
AF318573.1 GI:12802528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Sequence of Bovine Herpesvirus 4, a Bov Identification of an Origin of DNA Replication J. Virol. 75 (3), 1186-1194 (2001)
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1 (bases 1 to 108873)
2 immermann, W., Broll, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 108873)
Zimmermann, W., Broll, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein pBo1"
/protein_id="AAR07921.1"
/db_xref="GI:12802529"
/translation="MsDDYSMYAFGRKRTRQDLNNSAGGNEVCCAVLREKNHNVSAGC
CAVKRNNSFHHSLPGMWP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="long unique region; LUR" complement(445. .633) /note="ORF Bol"
                                                                                                                                                                                                                                                                                  /product=""-"FGAM-synthase"
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/protein_id="AAK07922.1"
/db_xref="01:12802530"
/db_xref="01:12802530"
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/translation="MDTSPSIQLCFFVSRRAPLSNECQVIQOFTSDGQLPLTSVPLQY
/translation="MDTSPSIQLFFVSRRAPLSNECQVIQOFTSDGQLPLTSVPLQY
/translation="MDTSPSIQLFFVSRRAPLSNecqvique"
/tran
                                                                                                    POHGPOT I VNONFCKTAY I VPVDYWI PEISTYTLSSGHMTDTGLAYTYGOLOVAPRDN
LLKEILYNSDAOMEGNVEYSSOLGI ASTYS I TYSPRSSY ELPPYTDI KUDAYMINNRCC
SLPCTOGYFFPI VESHLPLDSVPEGP I AFTGAVKOFSRNITTDL PETRHKI NI Y COFT
FTSSHEDSGREDVRCLIGALKYLMSF LAPSOVKOI SAVKVCETMHAKLLSVCQGI YGI K
I YQSALPPPLNTGLLPETASNRQONMTMI KOHFLNI VAPI VLVA I EAT PDNTTDTVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bovine herpesvirus 4"
/db_xref="taxon:10385"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                  AGČATHGCOYKVLGRRTOKPHTHTVKDKGEONVREKTSLKRYSPSYPLSTTNKLOKOS
ENWQDSSMEWDTLPSLSYTLLETLKHPAVGCKDFTVKHTDRLSSGRVAQQQGTGARDT
PISDYSILVSDLSLAAAPDRGSENPWATAESLDDLPLVNNEPVPPGICSAIGECFPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="tegument protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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VWLPISTEYHTFGTVISQLFRDSPSGHIINIDPLYVKKLITVTKHLINHESIISCHDV
GCGGLITACFEMAYAGGASIALTVPQOEDPVLFITSETTPGLMVEVRVVKVSTVKHLE
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LVSTFTDKTVKIVTDTTNVFGICLIGATNIEDATLGDKAISMYTKHNSYLVGELKKLI
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AVALQSMKGSLLPGWIQGTHLGFAHPSETYMEMLSTHGMVATQFYGADISAGPALTYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNPTAGYTISGLCSADGRHLALLHDPGLSNNLWQWPHIPKMTPPLKVSPWKRMFLDLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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/note="ORF Bo2; BORFA2"
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                                                                                                                                                               VGTÄASSDMCNLCQGKKPAVCINTLFYRLRDRFPPIITSHRRDPYIITGSVGMYNDLD
ILGNFASFREKEDEGAQVEEVQKYTYWQLTQTLLEKLEGMGIKDTTPPEKLVSDIPSF
IKVFKDIDAHVDTEVLKFINCMVKNNINFRETIKSIHHVIQYCCNVFAQPPCPVFLQL
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                                                                            YYKSILTIIODVCLENCMMYEODNSSMGMGPTEWLKMHYQTLWTNFKGCCFDRGVLTG
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SEAIQSGFLKSGSKKDNYIVTGPYMKFLNIYIKIMFFQTKMSSLFMWHTFSTKKQIPL
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KLRPIITVPMVINKYTGINGNNGIFHCGNLGYFMGRGVDRNLIFENAPFKRQSTNAYM
                             STTLHCLVPTYRTVPGEEYPHVLENEEFLGTEQYLKLVQNRTAQIVQATLKEDVAQMG
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CDS

CDS

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/db\_xref="GI:12802535"

/gene="gB" /note="ORF 8"

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gene
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FSCGCEVFESNVNASTRFIIDNERFSTFGWYSCSNPHFISQRIDSTTDLECGGGDLQ
FHEEDQQWPPYINSFDIECIGEQGFPCATKDEDLVIGISCIIWTVCSESEPONILL
FREEDQAMPYYTMSFSILLRDNIDFYTGYNAMATTETTTTV
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LNCHMSTINETLEETVKKENKSHIRDGEVKYYKTNGGLELIWQAMKPLNLSEHTNYTI
ERNNRTGKKSROKRSVDTKTEFOGAKGLSTAVVQYAYDHLRTSMHHILEELTKTWCRED
KKDNLMWYELSKINPVSVMAAIYGKPVÄVKAMGDÄFMVSECINVDQASVNIHKSMRTD
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GLTENINRYFSQPLIYAEPGWFPGIYRVRTTVNCEVVDMYARSVEPYTHFITALGDTI
EISPFCHNNSQCTTGNSTSRDATKVWIEENHQTVDYERRGHPTKDKRIFLKDEEYTIS
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TFDPSPGNDTSETHQKYV"
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EYNYYTQKLASLREDLDNTIDLNRDRLVKDLSEMMADLGDIGKVVVNTFSGIVTVFGS
IVGGFVSFFINPIGGVTIILLLIVVVEYVFIVSRRTNNMNEAPIKMIYPNIDKASBOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGELFRFDLDQTCPDTKDKKHVEGILLVLKKNIVPYIFKVRKYRKIATSVTVYRGWSQ
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//db_xref="G1:1280257"
//db_xref=
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PIPGFYNTPILVDFASLYPSIIQAHUCYSTMIQDQDUHLHLHLKPDDYETFHLSTGP
IHFWKQHKTKSLLSTLITAMLAKKTIRKELANCDDGPMKTILLXQQLAIKTVTCNSVY
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KVYSDGLPVGFMKVIDVLNNSYAALATGKVSVESLFSTELSREFGEKKTTTLPHLTY
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                                                                                                                                                                                                                                                                                                                         EDSMNVÄTLGENIIYSRCHLNLKSENTPSPMDTP"
complement(18848. .19345)
/note="ORF Bo4; short ORF of immedia
RNA"
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gamma-herpesviruses"
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KLNTVAKHCMGTQKEDVTYKEIPSLFRSGEAGRARIGSYCVLDSVLVLDLLKYFNIHV
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14184. .172(
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14.3%;
Score 194.8; DB 58; Pred. No. 1.6e-36;
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                                                                                                                                                                           cccagttgtactggatctcaccttcgaagcgtgtgtatttatggagctgcagaattaagg 1197
                                                                                                                                                                                                                    ATCGCCAGGCTCGTCAAGTGGCAGTACCACGAGGGAGATGTCAGCATGGGGGGCGCCTTAT 108455
                                                                                                                                                                                                                                                                                                                         ccaggaatacctggggagatttccagatcagcccaggatg---tgtctgatctgcagagt 1092
                                                                                                                                                                                                                                                                                                                                                                    GAATGGGTCAAAGACACCTATAGCCCCGACGAACACCTCTGGGCCACCCTTCAGCGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               gttttaagtcaagcatttgttaaatatattttcaacaactccatcgttcaagactttttt 975
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                                                                                          tggcttatcaaagatggacattggtttgctaataaatttgattctaaggtggaccctatc 1257
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                                   ttgattaaatgcttggcagaaaagct
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                                                                      TGGATTCTCCAGAACCATCACCTCTTGGCAAACAAGTTTGACCCGAGGGTGGATGATAAC
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  GAGCCGGTGGTCTATGGTGGAATCTCCCGGCTCCAGGCTGACCTGAACTGCATCAAAGAC
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                         gaggctgtggaatatgcccacatttccagactccaggctgatttaaattgcttgtcggac
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AB037597.1 GI:9650955
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Mus musculus IGnT A mRNA for
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Direct Submission
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pdpravdllhwskdffspdehfwvtlmripgypgsmpnaswfgnlravkwmmmeakh
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/protein_id="BAB03496.1"
/db_xref="GI:9650956"
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                                                                                                          Schwientek,T. and Clausen,H.

Udp-n-acetylglucosamine: galactose-g(b)1,3- n

udp-n-acetylglucosamine-g(a)-r/(glcnac to galnac)

-acetylglucosaminyltransfaras e, c2gnt3

Patent: WO 0114535-A 14 01-MAR-2001;

Schwientek, Tilo (DK); Clausen, Henrik (DK)

Schwientek, Tilo (DK); Clausen, Henrik (DK)
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1317)
                                                                                                                                                                                                                                                                                                                                  AX087948.1
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WO0114535
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99143102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens core 2/core (C2/4GnT) mRNA, complete AF038650
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YGAGDLNWMLQNHHLLANKFDPKVDDNALQCLEEYLRYKAIYGTEL"
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beta-1,6-N-acetylglucos
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                                                      2128 bp mRNA PRI 31-1
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complete cds.
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TTGAAAGGCTACTGCGAGCTGTGTATGCCCCCTCAGAACATATACTGTGTCCATGTGGATG

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                            tgaccagtgattgtgacatttatcagactctaagaggttatgctcaaaagcttgtctcaa
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517; Conserv
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Yeh, J.C., Ong.E. and Fukuda, M.

Molecular cloning and expression of a novel beta-1,

Molecular cloning and expression of a novel beta-1,
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Submitted (28-0CT-1998) Glycobiology Program, The Burnham
Institute, 10901 N. Torrey Pines Rd., La Jolla, CA 92037,
Location/Qualifiers
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YGAGDLWMMLQNHHLLANKFDFXVDDNALQCLEEYLRYKAIYGTEL"
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/db_xref="taxon:9606"
/tissue_type="brain"
/dev_stage="fetus"
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Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 174956 bases at least Q40
Consensus quality: 170052 bases at least Q30
Consensus quality: 172655 bases at least Q20
Insert size: 168000; agarose-fp
Tnsert size: 179683; sum-of-contigs
Quality coverage: 3.76 in Q20 bases; sum-of-contigs
Quality coverage: 3.85 in Q20 bases; sum-of-contigs
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Homo sapiens chromosome 15 clu
SEQUENCE, 24 unordered pieces
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Submitted (04-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jul 16, 2000 this sequence version replaced di.722107/
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Waterston, R. H.
The sequence of Homo sapiens clone
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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J97: contig of 6762 ...

68252: contig of 7955 bp in length
68352: gap of unknown length
75761: contig of 7409 bp in length
75761: contig of 7409 bp in length
84055: contig of 8194 bp in length
84055: contig of 8194 bp in length
84155: gap of unknown length
94092: contig of 10037 bp in length
94092: contig of 15430 bp in length
93 109722: contig of 15430 bp in length
109822: gap of unknown length
125338 125337: gap of unknown length
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125338 142872: contig of 15415 bp in length
142873 159682: contig of 17535 bp in length
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22457. .26948
/note="assembly_name:Contig31"
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/db_xref="taxon:9606"
/chromosome="15"
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53436. .60197
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75862. .84055
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36474. .41562
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34156. .94192
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/note="assembly_name:Contig43"
125338 ...142872
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159783. .181983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine herpesvirus 4 beta-1,6 (BORFF3-4) gene, complete cds AF231105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-FEB-2000) Immunology-Vaccinology, University of Liege, Faculty of Veterinary Medicine B43bis, Liege B-4000, B Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vanderplasschen, A., Mar
Hiraoka, N., Yeh, J.-C.,
and Pastoret, P.-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Pastoret, P.P.

A multipotential beta -1,6-N-acetylglucosaminyl-transferase encoded by bovine herpesvirus type 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 2017)
Vanderplasschen, A., Markine-Goriaynoff, N., Lomonte, P.,
Hiraoka, N., Yeh, J.C., Bureau, F., Willems, L., Thiry, E.,
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Bovine herpesvirus 4
Viruses; dsDNA viruses,
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                                       WATLQRAPWMPGSVPSHPKYHISDMTAIARLVKWQYHEGDVSMGAPYAPCSGIHRRAI
CIYGAGDLYWILQNHHLLANKFDPRVDDNVLQCLEEYLRHKAIYGTEL"
                                                                                               /translation="MKMAGWKKKLCPGHHLWALGCYMLLAVVSLRLSLRFKCDVDSLD
LESRDFOSGHGRDMLYMSLKLDAKRSINGSGITRGDGEAVVALLDNLEVKKRRPLT
DTYYLNITRDCERFKAGRKFIQFDLSKEELDPFIAYSMVYHKIENFERLLRAVYSPO
NIYCYHVDVKSFETFKEAVKAIISCFPNVFMASKLVPVVYASWSRVQADLNCMEDLLQ
SSYSWKYLLNTGGTDFPIKTNAEMVLALKMLKGKNSHESEVPSESKKNRWKYXYEVTD
                                                                                  SSYSWKYLLNTCGTDF9IKTNAEMYLALKMLKGKNSMESEVPSESKKNRWKYRYEVTD
TLYPTSKIKDP9PDNLPMFTGNAYFVASRAFVQHYLDNPKSQILVEMYKDTYSPDEHL
                                                                                                                                                                                             /product="beta-1,6-N-acetylglucosaminyltransferase"
/protein_id="AAF72001.1"
/db_xref="GI:8096689"
                                                                                                                                                                                                                                                                                       pBORFF3-4"
                                                                                                                                                                                                                                                                                                        /function="forms core 2, core 4, and I br.
/note="last ORF at the right end of the L
Homo sapiens core 2
beta-1,6-N-acetylglucosaminyltransferase,
                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BORFF3-4"
227. .1549
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227. .1549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bovine herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                       /gene="BORFF3-4"
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C., Bureau,F., Willems,
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,L., Thiry,E.,
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Fukuda,M.
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Fukuda,M.
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                                                               ttgattaaatgcttggcagaaaagct
                                                                                                                           TGGATTCTCCAGAACCATCACCTCTTGGCAAACAAGTTTGACCCGAGGGTGGATGATAAC
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                      1515
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 2393)

1 (bases 1 to 2393)

Magnet, A.D. and Fukuda, M.
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Institute, 10901 North Torrey Pines Road, La Jolla,
Location/Qualifiers
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Direct Submission
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Submitted (30-NOY-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 4, 2000 this sequence version replaced gi:11322778.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is not the entire insert of clone RP11-560019 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-421M1 is at 87537 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/HGP/Chr6
RP11-360019 is from the library RPCI-11.2 constructed at the
Roswell Park Cancer Institute by the group of Pieter de Jong.
further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACe3.6
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3783...3077
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/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                               /note="AluY repeat: 9704. .10003
                                                                                                                                                                                                                                                                                                     /note="MIR repeat: 8679. .8970
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 1. .282 of consensus" 6304. .6357
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1036. .1404
                                                                                               /note="AluSg repeat: 10767. 10860
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/note="MIR repeat: matches
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/note="AluSx repeat:
11522. .11570
                                11094.
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/note="AluSq repeat:
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                                                                                 /note="L1ME2
                                                                                                                                                                                                                                                                                                                                                        /note="L1MD3 repeat: matches 7076. .7738 of consensus"
                                                                                                                                                                                                                                                      note="MIR repeat:
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                .304 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MER82 repeat: matches 1. .96 of consensus"
11794. .12114
/note="LLME2 repeat: matches 5315. .5644 of conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1M4 repeat: matches 2691. .2758 of consensus"
|2934. .13237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MSTA repeat: matches 238. .370 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2157. .1224

'note="L1PA11 repeat: matches 6095. .6164 of consensus"

.2246. .12683
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                              note="Alusx repeat: matches 1. .284 of consensus"
                                                                                                                                                 note="AluJb repeat: matches 130. .148 of consensus"
23736. .24036
                                                                                                                                                                                     note="Alusp repeat:
23717. .23735
                                                           note="L2 repeat: matches 2336. .2394 of
                                                                                                 'note="AluJb repeat:
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18547
te="MER200 repeat: matches 26. .218 of consensus"
14. .19001
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17. .14815
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79. .23404
repeat: matches 1. .130 of consensus"
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7. .22496
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2. .22018
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                                                                                                                                                                                                                                                                                    e="L1MA6 repeat: matches 5862. .6300 of consensus"
1. .23278
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9. .19615
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7. .20715
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1. .18080
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repeat:
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                                                                                                  matches 148. .301 of
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 matches 5893.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Aiusx : 34121. .34431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28553. .28845
'note="AluY re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;2542. .32606
/note="L2 repeat:
32885. .33161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="AluSp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="FLAM_
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26934...27236 /note="AluSp repeat: matches 1...304 of consensus" 27466...27765 /note="Alux repeat: matches" /note="AluSx repeat: matches 1. .308 of consensus" note="L1MC/D repeat: matches 5761, .5796 of consensus" 28281, .28552 'note="AluSx repeat: matches 1. note="AluSx repeat: matches 1. .296 of consensus"
0335 .30639 e="AluJb repeat: matches 42. .312 of consensus" e="Alusx repeat: matches 10. A repeat: matches 1. matches 2679. matches 1. matches 4. .293 of consensus" .305 of consensus" .313 of consensus" .2746 of consensus" .298 of consensus' .133 of consensus"

Score 187.4; DB 90; Pred. No. 9.5e-35; 0; Mismatches 306; Indels Length 87636 6; Gaps

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ccagcacaatatttactgcatccattatgatcgtaaggcacctgataccttcaaagttgc 40310

catgaacaatttagctaagtgcttctccaatattttcattgcttccaaatttagaggctgt 584 40370

TGTCTATGGGGGGATCTCCAGGCTCAGGCTGACCTGAACTGCCTGGAAGACCTTGTGGC 40430 ggaatatgcccacatttccagactccaggctgatttaaattgcttgtcggaccttctgaa 644

CTCTGAAGTTCCCTGGAAGTATGTCATCAACACCTGCGGGCAAGACTTTCCCCCTGAAAAC 40490 gtcttcaatccagtggaaatatgttatcaacttgtgtgggcaagattttcccctgaagtc 704

CAACAGGGAAATAGTTCAGTATCTGAAGGGATTTAAAGGGAAAAATATCACCCCCGGAGT aaattttgaattggtgtcagagttgaaaaaactcaatggagcaaatatgttggagacggt 764

40550

GCTGCCTCCTGACCACGCTGTTGGACGGACTAAATACGTCCACCA-----AGAACTGTT 40604 gaaacccccaaacagtaaattggaaagattcacttaccatcatgaacttagacgggtgcc 824

AAACCACAAAAATTCCTACGTGATTAAAACAACAAAATTAAAAACTCCTCCTCCTCATGA 40664 ttatgaatatgtgaagctaccaataaggacaaacatctccaaggaagcaccccccataa

tttcaacaactccatcgttcaagactttttttgcctggtctaaagacacatactctcctga 1004 cattcagatatttgttggcagtgcttattttgttttaagtcaagcatttgttaaatatat CATGGTGATTTACTTTGGCACGGCCTACGTGGCTCTCACAAGGGACTTTGCTAACTTCGT 944 40724

40784

REFERENCE AUTHORS TITLE

Sims,S.
Direct Submission

JOURNAL

COMMENT

KEYWORDS SOURCE ORGANISM

Homo sapiens

/ERSION ACCESSION RESULT 1 AL138877 LOCUS

DEFINITION

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40785 1005

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tgagcacttttgggctaccttgattcgggttccaggaat 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 175144; sum-of-contigs
Insert size: 171752; 11.8% error; agarcse-fp
Quality coverage: 3.86x in Q20 bases; sum-of-contigs Quality
coverage: 4.04x in Q20 bases; agarcse-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5 sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 168731 bases at least Q40 consensus quality: 171090 bases at least Q30 consensus quality: 172929 bases at least Q20 consensus quality: 172929 bases at least Q20
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Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL138877.4 GI:9863512
HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: bAl5I14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
   8250 8349; gap of
8350 8349; gap of
100 bp
26088; contig of 17739 bb in length
26089 26188; gap of
26189 3312; contig of 7724 bp in length
33913 34012; gap of
58934 5893; contig of 24881 bp in length
5894 5893; gap of
63787 63886; gap of
69120 69119; contig of 5233 bp in length
63787 63886; gap of
69220 75187; contig of 5233 bp in length
69220 75187; contig of 5968 bp in length
81894 81993; gap of
81994 81993; contig of 5968 bp in length
81894 81993; contig of 506 bp in length
81894 81993; contig of 306 bp
81994 81993; contig of 308 bp
81994 81995; contig of 308 bp
81556; contig of 308 bp
87557 87656; gap of
87525; contig of 308 bp in length
87557 87656; gap of
87657 97225; contig of 308 bp
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84258: gap of 100 bp
87556: contig of 3298 bp in
87656: gap of 100 bp
97225: contig of 9569 bp in
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Best Local Similarity
Matches 387; Conserv
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                   405 ttctttggttgtccacaaagatgcaattatggttgaaaggcttatccatgctatatacaa 464
                                                                                                                                                                                345 totaagaggttatgotcaaaagcttgtotcaaaggaggagaaaagcttcccaaatagcota 404
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97326 104701: contig of 7376 bp in length

104702 104801: gap of 100 bp

104802 128525: contig of 23724 bp in length

128526 128625: gap of 100 bp

138526 137228: contig of 8603 bp in length

137229 137328: gap of 100 bp

137229 176544: contig of 39216 bp in length.

100 bp
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97326. 104701
/note="assembly_fragment:01036
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/note="assembly_fragment:00557
fragment_chain:1"
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137329. .176544
/note="assembly_fragment:01031"
/note="assembly_fragment:01031"
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/note="assembly_fragment:00061
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fragment_chain:1"
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/db_xref="taxon:9606"
/chromosome="6"
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fragment_chain:1"
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/clone_lib="RPCI-11.1"
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fragment_chain:3"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:2"
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                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                 Score 187.4; DB 7
Pred. No. 9.9e-35;
                                                                                                                                                                                                                                                                                  Mismatches 306;
                                                                                                                                                                                                                                                                                                                                                             DB 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1411 others
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preserved

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Db 102271
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                 TITLE
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

be preserved

1282 1381:

1281: contig of 1281 bp in length 1: gap of 100 bp 2899: contig of 1518 bp in length 9: gap of 100 bp

2999:

2 5781: gap of 100 2 8351: contig of 2

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35694: gap of 40148: con

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NOTE: This is a 'working draft' sequence. It currentle consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record

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Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced 91:6978227.
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Stojanovic, N.
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                                                                                                                                                                                                                                                                                                                                                            Insert size: 208000; agarose-fp Insert size: 194088; sum-of-contigs Quality coverage: 3.7 in Q20 bases; Quality coverage: 4.0 in Q20 bases;
                                                                                                               Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 consensus quality: 180581 bases at least Q40 consensus quality: 189581 bases at least Q20 consensus quality: 192532 bases at least Q20
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Center clone name: 391_I_2
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67812 67912 74070: contig of 6159 bp in length
67917 74070: contig of 6159 bp in length
74071 74170: gap of 100 bp
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score greater than or equal to the score of the result being printed,
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Copyright (c) 1993 - 2000 Comp
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## ALIGNMENTS

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X MEDLINE=4042310.

A Schwientex T., Yeh J.C., Levery S.B., Neuron.

AN A Kessel A.G., Fukuda M., Clausen H.;

AN A Kessel A.G., Fukuda M., Clausen H.;

AT "Control of O-glycan branch formation. Molecular cloning and characterization of a novel thymus-associated core 2 betal,6-N-RT acetylglucosaminyltransferase.",

RI J. Biol. Chem. 275:11106-11113(2000).

BMBL, AF132035; AAF63156.1; --

DR Interpro; IPR003406; .

DR Pfam; PF02455; Branch; 1.

DR Pfam; PF02455; Branch; 1.

RW Transferase. Glycosyltransferase.

KW Transferase. Glycosyltransferase.

KW SEDUENCE 453 AA; 53052 MW; B43794D4427F41CA CRC64;
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Q9P109;
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MEDLINE=20219156; PubMed=10753916;
MEDLINE=20219156; PubMed=10753916;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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2 BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE 3.
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Mismatches 0;
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JT 01-MAX-1999 (TrEMBLrel. 10, Created)
DT 01-MAR-2091 (TIEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TIEMBLrel. 16, Last annotation update)
DE BETA-1,6-N-ACETYLIGLUCOSAMINYLITRANSFERASE.
GN C2/4GNI.
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC Eukaryota; Metazoa; Chordata; Catarrhini; Hominida.
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RA Schwientek T., Nomoto M., Levery S.B., Merkx G., van Kessel RA;

RA Bennett E.P., Hollingsworth M.A., Clausen H.;

RT "Control of O-glycan branch formation. Molecular cloning of encoding a novel betal,6-N-acetylglucosaminyltransferase form 27 and core 4.";

RT 2 and core 4.";

RL J. Biol. Chem. 274:4504-4512(1999).

REMBL; AF102542; AAD10824.1;

REMBL; AF038650; AAD21525.1;

R InterPro; IPR003406: -
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Yeh J.C., Ong E., Fukuda M.;
"Molecular cloning and expression o
acetylglucosaminyltransferase that
branches":
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Transferase; Glycosyltransferase.
SEQUENCE 438 AA; 50883 MW; 1FF0A7B451C88407
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STSPFVRN-RYTHVKDEVRYEVNCSGIY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVA
                                                                                                                                                                              SQSQYCRNILYNFLKLPAKRSINCSGVTRGDQEAVLQAILNNLEVKKKR-EPFTDTHYLS
                                                                           LTRDCEHFKAERKFIQFPLSKEEVEFPIAYSMVIHEKIENFERLLRAVYAPQNIYCVHVD
                                                                                                                         MTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYD
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Pred. No. 1.5e
70; Mismatches
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ns core 2, core 4,
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Best Local S
Matches 177
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STRAIN-SPRACUE-DAWLEY; TISSUE-HEART;
MEDLINE-96013636; PubMed-7560067;
MISHIO Y., Warren C.E., Buczek-Thomas J.A., Rulfs J.W., King G. Aiello L.P., Feener E.P., Miller T.B.Jr., Dennis J.W., King G. "Identification and characterization of a gene regulating eng glycosylation which is induced by diabetes and hyperglycemia specifically in rat cardiac tissue.";
J. Clin. Invest. 96:1759-1767(1995).
EMBL; S79777; AAB35697.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q64165 PRELIMINARY; PRT; 428 AA. Q64165; 01-NOY-1996 (TrEMBLrel. 01, Created) 01-NOY-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update ENZYMATIC GLYCOSYLATION-REGULATING GENE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003406; -.
Pfam; PF02485; Branch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400
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NSIVQDFFAWSKDTYSPDEHFWATLIRVPGIPGEISRSAQ-DVSDLQSKTRLVKWNYYEG
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428 AA; 49
                                                                                          KRYTVVDGKL-TNTGVVKAQPPLKTPLFSGSAYFVVTREYVGYVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TPHDYINMTRDCASFIRTRKYIMEPLTKEEVGFPIAYSI 127
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Sciurognathi; Muridae;
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; Murinae; Rat
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proc. Natl. Acad. Sci. U.S.A. 97:5756-5761(2000).
EMBL; AF231105; AAF72001.1; -.
Interpro; IPR003406; -.
pfam; PF02485; Branch; 1.
Transferase; Glycosyltransferase.
SEQUENCE 440 AA; 50701 MW; 71B9C3B6B4A949BD CRC64;
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O9IZK2.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
BETA-1.6-N-ACETYLGLUCOSAMINYLTRANSFERASE.
BORFF3-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses,
Gammaherpesvirinae.
NCBI_TaxID=10385;
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   035981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=V. TEST;
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                                                                                                                                                                                                                   MNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKS
                                                                                                                                                                                                                                                                                                YTHVKDEVRYEVNCSGIY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQT
                                                                                                                                                                                                                                                                                                                           168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FF----
                                                                                                   SAQDVSDLQSKTRLVKWNYYEGFF----
                                                                                                                                       IQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIPGEI-SR
                                                                                                                                                                                                         VKAIISCFPNVFMASKLVPVVYASWSRVQADLNCMEDLLQSSVSWKYLLNTCGTDFPIKT
                                                                                                                                                                                                                                              QRKFIQFPLSKEELDFPIAYSMVVHEKIENFERLLRAVYAPQNIYCVHVDVKSPETFKEA
                                                                                                                                                                                                                                                        LRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKNIQKEMEWAQDTYSPDEFLWATIQRIPEVPGSLPSSHKYDLSDMNAVAREVKWQYFEG
                                                  NKFDPRVDDNVLQCLEEYLRHK
                                                                   NKFDSKVDPILIKCLAEKLEEQ
                                                                                      PKYHISDMTAIARLVKWQYHEGDVSMGAPYAPCSGIHRRAICIYGAGDLYWILQNHHLLA
                                                                                                                            LPMFTGNAYFVASRAFVQHVLDNPKSQILVEWVKDTYSPDEHLWATLQRAPWMPGSVPSH
                                                                                                                                                                  NAEMVLALKMLKGKNSMESEVPSESKKNRWKYRYEVTDTLYPTSKI---
                                                                                                                                                                                    NFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHN
                                                                                                                                                                                                                                                                                     YNSLKLPAKRSINCSGITRGDQEAVVQALLDNLEVKKKR-PPLTDTYYLNITRDCERFKA
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQ
                                                                                                                                                                                                                                                                                                                          Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                  38.7%;
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                                                                                                                                                                                                                                                                                                                       72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA
                                                                                                                                                                                                                                                                                                                        Score 848; DB
Pred. No. 1.8e-
72; Mismatches
                                                                   393
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stage;
                                                                                                        -YPSCTGSHLRSVCIYGAAELRWLIKDGHWFA
                                                                                                                                                                                                                                                                                                                                  848; DB 14;
No. 1.8e-58;
  428
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on update)
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L., Thiry
                                                                                                                                                                                                                                                                                                                           124;
                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                  KDPPPDN
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           Homo
   Eukaryota;
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Query Match
Best Local S
Matches 166
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O1-JAN-1998 (TremBLrel. 05, Creat O1-JAN-1998 (TremBLrel. 05, Last O1-MAR-2001 (TremBLrel. 16, Last GLUCOSAMINYL (N-ACETYL) TRANSFERZ ACETYLGLUCOSAMINYLTRANSFERZASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 272:27246-27252(1997).
EMBL, D87333; BAA22999.1; -.
EMBL, D87332; BAA22998.1; -.
MGD; MGI:95676; Gcntl.
InterPro: IPR003406; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                O9HCV8:
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DJ1153D9.2 (A NOVEL PROTEIN SIMILAR TO BETA 1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE.) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003406; -.
pfam; pF02485; Branch; 1.
Transferase, Glycosyltransferase.
SEQUENCE 428 AA; 49831 MW; F0D10A6ADB23B92C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C; TISSUB-SUBMAXILLARY GLAND,
MEDLINE-98001705; PubMed-9341170;
Sekine M., Nara K., Suzuki A.;
"Tissue-specific regulation of mouse core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
[1]
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                    DJ1153D9
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 sapiens
                                                                                                                                                                                                                                                                                                                              DVSDLQSKTRLVKWNYYEGFF-----YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKF
                                                                                                                                                                                                                                                                                                                                                                                                   FVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIPGEI-SRSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAKCESNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDEPLKSNFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIVEPLTKEEVGFPIAYSIVVHHKIEMLDRLLRAIYMPQNFYCIHVDRKAEESFLAAVQG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAQKLYSKEEKSFPIAYSLYVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNN 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDPYSNVNCTKILQGDPEEIQKVKLEILTVQFKKRP--RWTPHDYINNTRDCASFIRTRK 108
                                                                                                                                                                                                                                    DIDVDPFAIQCLDEHLRRK
                                                                                                                                                                                                                                                                   DSKYDPILIKCLAEKLEEQ
                                                                                                                                                                                                                                                                                                     FSGSAYFVVTREYVGYVLENENIQKLMEWAQDTYSPDEFLWATIQRIPEVPGSFPSSNKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVRKLKCSTAENNLETEKMPPNKEERWK-----KRYAVVDGKL-TNTGIVKAPPPLKTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IASCEDNVEVASQLESVVYASWSRVKADLNCMKDLYRMNANWKYLINLCGMDFPIKTNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166;
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66; Conservative
                                                                                                                                             PRELIMINARY
(Human)
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Rodentia;
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05, Last sequence update)
16, Last annotation update)
TRANSFERASE 1, CORE 2 (BETA
                                                                                                                                                                                                                                      421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 833; DB 11;
Pred. No. 2.6e-57;
5; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                             PRT;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
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Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

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Best Local S
Matches 99
Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q19730 PRELIMINARY;
Q19730;
Q19730;
Q1-NOV-1996 (TIEMBLIGH: 0
01-NOV-1996 (TIEMBLIGH: 0
01-MAR-2001 (TIEMBLIGH: 1
F22D6:11 PROTEIN:
                                                                                                                                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2000) to t
EMBL; AL109806; CAC03741.
NON_TER 1 1
NON_TER 314 314
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                                                           Pfam; PF02485;
SEQUENCE 445
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
MCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; NCBI_TaxID=9606; [1]
                                                                                                    Nature 368:32-38(1994).

EMBL; Z71262; CAA95817.

InterPro; IPR003406; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
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                                                                                                                                                                       elegans.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSEL
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99; Conservative
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                                                             Branch; 1.
AA; 51330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oda; Chromadorea;
Caenorhabditis.
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Pred. No. 4.5e-32;
1; Mismatches 82
    Score
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01-JUL-1997
01-MAY-1999
01-MAR-2001
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Caenorhabditis.
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EMBL, 283102; CAB05469.1; JOINED
EMBL; AL032664; CAB05469.1; JOINED
EMBL; AL032664; CAA21769.1; JOINED
EMBL; 283102; CAA21769.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003406; -. Pfam; PF02485; Branch; 1.
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SEQUENCE 425 AA; 4
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(TrEMBLrel. 16, Last annotation update)
L PROTEIN C54C8.11.
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                                                                                                                                                                                                                                                                                         Score 313.5; DE
Pred. No. 1.3e-1
0; Mismatches 1
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RESULT OCCURRENCE OCCU
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Best Local S
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01-JUL-1997 (TrEMBLrel. (
01-MAR-2001 (TrEMBLrel. 1
T15D6.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
T. 2. M. Gontiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            002314;
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                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003406; Pfam; PF02485; Brancl SEQUENCE 401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340
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                                                                            SRYQQYVNRAPVKCKGYYYRLSCVFGVYDLPNLINRHELVAHKLYFSYQPAAFMCLVENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFFYP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LPFEFYRLNRKRPWSSPLPLYKTSL---SATF--SRKSANFMVNSEKVLEQIDFLRGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAKLPSDWKYFQYLSGVDAPLKSNLEMIRILKALNG-----
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EVPLSEEEARFPLSYGLLVYKELSQVLFMLSSIYQPQNEYCIAVGENSASTFLILLEELS
                                              QKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLA 142
                                                                                                                                                 THVKDEVRYEVNCSGIYEQEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYA
                                                                                                                                                                                                                                                                                                                                                                                                              Z83125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                    Branch; 1.
AA; 45608 MW;
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16,
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Caenorhabditis.
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Last sequence
Last annotation
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                                                                                                                                                                                                        68;
                                                                                                                                                                                                   Score 296; DB
Pred. No. 2.7e
58; Mismatches
                                                                                                                                                                                                                                                                                                                                      E1D3F8AD84C0873D CRC64;
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2.7e-15;
hes 157;
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                                                                                                                                                                                                                                                         Length 401;
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                                                                                                                                                                                                        56;
                                                                                                                                                                                                        Gaps
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80 A0

FVRNRYTHVKDEV----RYEVNCSGIYEQEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCD

FLKSICTTASDSYLLDNMEINCSNIL--KGYKTNEKLDIMHLDII---EEQLFSCTNKCQ

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17 40 74 95

TLKTLFRENTNPMSAEEKHFPLSYGMLVYKDLPQVTPARMFIKLHFLEINLQVLFLLSSI

IYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDA-----

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RESULT
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                      Matches
                                          Query Match
Best Local
                                                                                                                                  Natúre 368:32-38(1994).
EMBL; Z71262; CAA95816.1; -
InterPro; IPRO03406; -
Pfam; PF02485; Branch; 1.
SEQUENCE 454 AA; 52822 M
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Q19729;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Couls
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston
Jones M., Kershaw J., Kirsten J., Laister N., Latteille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownk
Smaldon N., Smith A., Sonnhammer E., Staden R., Suiston J.,
This control of the 
                                                                                                                                                                                                                                                   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston F Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1996 (TremBLrel.
01-MAR-2001 (TremBLrel.
F22D6.12 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
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                      l Similarity 24.
99; Conservative
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                                                                                                                                            52822 MW;
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16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ
                         73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence
Last annotation
                      Score 291; DB
Pred. No. 7.9e
73; Mismatches
                                                                                                                                            FA0134DBF31D0925 CRC64;
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DB 7.9e-15;
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                           Indels
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Q20406;
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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F44F4.6 PROTEIN.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson is
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Waltson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C
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EMBL; Z37092; CAA85457.1; -.
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                              EEAEYPLAYGLVVYKTIVQVLTQMSLFYQPQHMFCITVDDQSPNEYKSVIQALFSCFPNM 182
                                                                                           ENIPLECNSVINGTENRRKISRARQWDWHFDWVEHEIFNSRNVCSTIDKYFNFTRIPSSR
-IFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDEPLKSNFELVSELK
                                                           EEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSN- 147
                                                                                                                                                                                                                                     PF02485; Branch; 1.
NCE 472 AA; 55412 MW;
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Pred. No. 1.3e
78; Mismatches
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Couls
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston
Jones M., Kershaw J., Kirsten J., Laister N., Latrelle P.,
Johnston J., Loyd C., Mcmurray A., Mortimore B., O'Callaghan
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Smaldon N., Smith A., Sonnhamer E., Staden R., Sulston J.,
Finerry Mileg J., Thomas K., Vaudin M., Vaughan K., Watterston R.
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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Pfam; PF02485; Branch
SEQUENCE 402 AA; 4
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Nature 368:32-38(1994).
EMBL; Z83125; CAB05621.1;
InterPro; IPR003406; -.
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Eukaryota: Metazoa: Nem
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KCFSNIFIASKLEAVEYÄHISRLQADLNCLSDLLKSSIQWKYVINLCGQDEPLKSNFELV
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                                            KVPLSEEEARFPLSFGLLVYKELSQVLFLLSSIYQPQNEYCIAVGENSAPAFLILLKELA
                                                                        QKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLA 142
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M. Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"1.2 M. Weinstock L., Wilkinson-Sproat J., Wohldman P.;"
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Eukaryota; Metazoa; Nemat.
Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                                          InterPro; IPR003406; Pfam; PF02485; Brancl SEQUENCE 459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McLay
                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
EMBL; Z81147; CAB03536.1;
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                                                                                                                                         IYLVEYSLSTSPFVRNRYTHVKDEVRYEVNCSGIY--EQEPLEIGKSLEIRRRDIIDLED
 RIIPHDHILRPLKNGVAFARIVYKDYELVEKQVQMSYHPQNSFCFAIDKKAPTRFKNQMR
                                                        KIEHFYSKTYRRRSETAHVDCGRILSGDKDYLQTVSG--ENRIPMVENPNPDMSCSAVMD
                                                                                                             VYYLMFS-SKSLFGRN-----
                                                                                                                                                                       106;
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                                                                                                                                                                       Similarity 22.8
06; Conservative
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Branch; 1.
AA; 53476
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Last sequence update)
Last annotation update)
                                                                                                                                                                    Score 245; DB Pred. No. 3.2e 74; Mismatches
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                                                                                                               -EQNSYALYNLRNENYQREAIINELRRDFAKIES
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   RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Harris N.L., Harvey S., Dahlke C., Ferraz C., Ferriera S., Fleischmann W.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshira N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshira N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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Q1-MAY-2000 (TIEMBLIFE1. 1
Q1-MAY-2000 (TIEMBLIFE1. 1
Q1-MAR-2001 (TIEMBLIFE1. 1
CG17771 PROTEIN.
CG17771 OR CG17772 OR ANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=IMAGINAL DISK,
Bessarab D.A., Sun H
Submitted (JUL-1995)
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MEDLINE=20196006; PubMed=10731132;
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SEQUENCE FROM N.A.
"TWAGINAL DISK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG17772 OR ANON-I2.
melanogaster (Fruit fly).
melanogaster (Fruit fly).
Metazoa; Arthropoda; Trachea
Neoptera; Endopterygota; Dir
Neoptera; Endopterygota; Dir
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Last sequence Last anno
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ota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -CASKYKRHNVCILGIEYLRSVASFPTLMFNKML
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b J.M.,
, Reese M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375
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Best Local S
Matches 89
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EMBL; BE003474; AAE47625.1; ...
EMBL; AE003474; AAE47626.1; ...
EMBL; AE003474; AAE47626.1; ...
F1yBase; Ebgn0015360; CG17771.
InterPro; IPR002889; ...
InterPro; IPR002889; ...
InterPro; IPR003406; ...
Pfam. De701073: ...
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O45866;

O1-JUN-1998 (TREMBLEGL O

O1-JUN-1998 (TREMBLEGL O

O1-MAR-2001 (TREMBLEGL O

T27E6.1 PROTEIN.
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
Science 287:2185-2195(2000).
Science 287:2185-2195(2000).
Science 287:2186-2186-25 DIFFERS FROM THAT SHOWN DUE TO A
SHORT FORM; ARE PRODUCED DIFFERS FROM THAT SHOWN DUE TO A
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Pfam; PF02485; Branch; 2.
PROSITE; PS00071; GAPDH; UNKNOWN_1.
               Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternative splicing; Hypothetical protein.

VARSPLIC 1 321 MISSING (IN SHORT ISOFORM)
SEQUENCE 876 AA; 99097 MW; A034F7584E59DB98 CRC64;
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                                                                                                                                                                                                                                                                                                   FKPEDWPRLQATEQKSLFFARKF----EPVINQAVLLQLEE----WLYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-NISKEAPPHNIQIFVGSAYFVLSQAFVKYIF----NNSIVQDFFAWSKDTYSPDEHFW
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                                                                                                                                                                                                                                                                                                                                                                          HTVLR----
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                                                                                                                                                                                                                                                                                                                                   -----ELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQQRDWITLP
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                                     Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5%; Score 231; DB 5; Length 8: 25.4%; Pred. No. 9.5e-10; cive 63; Mismatches 148; Indels
                                                                                                                                16,
06,
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Last sequence tast annotation
                                                                                                                                sequence update) annotation update)
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Best Local S
Matches 80
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Bonfield J., Burton J., Connell M., Copsey T., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003406; -. Pfam; PF02485; Branch; 1. SEQUENCE 454 AA; 52603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94150718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
                                 363
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les 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                   84 KLVSKEEKSFP----IAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMN 139
                                                                                                                                                                                                                                                                                   NLAKCESNIFI------ASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYYINLCG
                                                                                                                                                                                                                                                                                                                                 RILSRDHYLRPLENGVAFARVYYMDYELIEKHYEMSYHPQNGFCFAIDKKAAKEFKERMQ 169
                                                                                                                                                               KEAP---PHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFF-AWSKDTYSPDEHFWAT--L 304
                                                                                                                                                                                                 HDLITKSVYELEKIFNWLGGANDV-AIRPELGRLDK-----KHFKWDPMSLKLERNES
MAKSEHLMFNKVLPLFDYSIIECTAELL
                                 LIKDGHWFANKFDSKVDPILIKCLAEKL
                                                                 SDFLGMPGHFTDKCIKKGIITEGITRFAQWTHGD----QSKCASKKSRHGICIMGIEHLSM
                                                                                               IRVPGIPGEIS-RSAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLR-SVCIYGAAELRW
                                                                                                                                 EIDPVILNTTLKFAKGAVQSSLSRAAVDWMTRTVDLTTFIDQWNHGTYGVDEQFTQAFQI
                                                                                                                                                                                                                                 QDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNIS
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Search completed: August 2, 2001, 14:49:54 Job time: 299 sec

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Perfect score:
Sequence:
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(c) 1993
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VOO1_VACCC
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G6NT_BOVIN
BGIB_MOUSE
BGIB_HUMAN
YA54_METJA
WHI3_YEAST
BFR2_HUMAN
GAAP_HUMAN
YQB6_CAEEL
SYGB_HELPJ
SYGB_HELPJ
IF93_MOUSE
CLH1_HUMAN
CLH_BOVIN
CLH_BOVIN
CLH_BOF
SECA_PORPJ
CPV1_SHEEP
Y2.08_METJA
POLD_BORBU
CYGF_BOVIN
IF3A_HUMAN
SPOT_MYCGE
ATX1_FLAFA
DP3B_MYCGE
Y0.78_YEAST
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                EMBL; M97347; AAA35919.1; -. EMBL; L41415; AAA96661.1; -. PIR; A46293; A46293. MIM; 600391; -.
  Transferase; Glycosyltransferase;
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91 4.1 1077 1 DNZL_HOMAN 90.5 4.1 560 1 INRL_SHEEP 90.5 4.1 759 1 TEAL_YEAST 90.5 4.1 936 1 CYAR_YEARE 90.5 4.1 936 1 WSH4_HUMAN 90.5 4.1 936 1 YA14_MYCGE 90.5 4.1 1036 1 YA14_MYCGE 90.5 4.1 1036 1 YCF2_TOBAC 90.4 1 415 1 EFIG_YEAST 90 4.1 503 1 CPY2_PIG 90 4.1 1324 1 VGLZ_CYMAS 90 4.1 1324 1 VGLZ_CYMAS 90 4.1 1324 1 N188_YEAST	4.1 1077 1 DNZL_HUMAN 4.1 560 1 INR1_SHEEP 4.1 759 1 TEAL_YEAST 4.1 850 1 CYAA_YERPE 4.1 936 1 WSH4_HUMAN 4.1 1036 1 Y414_MYCGE 4.1 2380 1 YCF2_TOBAC 4.1 2180 1 EFIG_YEAST 4.1 503 1 CPV2_PIG 4.1 1324 1 VGL2_CVMAS 4.1 1324 1 N188_YEAST 4.1 1655 1 N188_YEAST
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<b></b>	1 DNZL_HUMAN P51530 1 INNI_SHEEP C28589 1 TEA1_YEAST P40127 1 MSH4_HUMAN P40127 1 MSH4_HUMAN P4753 1 YCF2_TOBAC P29547 1 Y411_MYCGE P29547 1 YCF2_TOBAC P29547 1 CPV2_PIG P29547 1 CPV2_PIG P39430 1 VGL2_CVMA5 P11224 1 VGL2_CVMA5 P11224 1 N188_YEAST P52593
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INZL_HOMAN INTL_SHEEP TEA1_YEAST CYAA_YEAPE WSH4_HUMAN Y4.14_MYCGE YCF2_TOBAC EF1G_YEAST CPV2_PIG GLMS_THEMA VGL2_CYMA5 N188_YEAST	P5.15.30 Q28589 P40128 P40127 O1.5457 O1.5458 P0.997653 P29547 P79430 Q94420 P52293

## ALIGNMENTS

Transmembrane; Signal-anchor;

stack;

Glycoprotein

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SEQUENCE
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DOMAIN
                                                                                                                                                            STRAIN-DBA/2;

Warren C.E., Scookler D.S., Dennis J.W.;

Warren C.E., Scookler D.S., Dennis J.W.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: FORMS CRITICAL BRANCHES IN O-GLYCANS.

-i- CAPALYTIC ACTIVITY; UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL-1,3-N-ACETYL-D-GALACTOSAMINYL-R = UDP + BETA-D-GALACTOSYL-1,3-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,6)-N-ACETYL-D-GALACTOSAMINYL-R.
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                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                     GCNT1
                                                                                                                                                                                                                                                                                                                                                           338
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NSKLERFTYHHELRRVPYEYV--KLPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVKYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHHKIEMLDRLLRAIYMPQNFYCVHVDTKSEDSYLAAVMGIASCFSNVFVASRLESVVYA
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49784
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Rodentia;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTE (POTENTIAL).

LUMENAL, CATALLYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 849.5; I
Pred. No. 4.2e-
70; Mismatches
                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB .
4.2e-55;
3s 129;
                                                                                                                      Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVNCSGIYEQEPLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                          ,6-N-
2 BRANCHING
                                                                                                                                 Euteleostomi;
                                                                                                                      Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN)
                                                                                                                       Mus
                                                                                                                                                                           ENZYME)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220
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                                                                                                                                                                                                                                                                                                                                                             392
                                                                                                                                                                                                                                                                                                                                                                                                     337
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9
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                                                                                                                                                                                         밁
                                                                                                                                                                                                             QΥ
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                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Golgi stack;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U19265; AAA60948.1; MGD; MGI:95676; Gcnt1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - - -
                                                   092180;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BETA-1,3-GALACTOSYL-O-GLYCOSYL-GLYCOPTEIN BETA-1,
ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE
(COREZ-GLCNAC-TRANSFERASE) (C2GNT) (CORE 2 GNT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase;
                                                                                                                                  G6NT
                                                                                                                                              BOVIN
          Eukaryota;
Mammalia; [
                                Bos taurus
                                                                                                                                                                                         403
                                                                                                                                                                                                               375
                                                                                                                                                                                                                                     343
                                                                                                                                                                                                                                                                                                                           229
                                                                                                                                                                                                                                                                                                                                               201
                                                                                                                                                                                                                                                                                                                                                                       169
                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                          320
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                                                                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                                                                                                                                                                       81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: GLYCOSYLATION.
SUBCELLULAR LOCATION: TYPE
SIMILARITY: TO I-BRANCHING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVRYEVNCSGIYEQEPLEIGK-----SLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRG
                                                                                                                                                                                                                                                                                                                                                                                                                             DDPYSNVNCTKILOGDPEEIOKVKLEILTVQFKKRP--RWTPHDYINMTRDCASFIRTRK 108
                                                                                                                                                                                                                                   LVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQI
                                                                                                                                                                                                                                                                                                                                                                       LAKCESNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFE
                                                                                                                                                                                                                                                                                                                                                                                                                 YIVEPLTKEEVGFPIAYSIVVHHKIEMLDRLLRAIYMPQNFYCIHVDRKAEESFLAAVQG
                                                                                                                                  BOVIN
                                                                                                                                                                                         DMDVDPFAIQCLDEHLRRK
                                                                                                                                                                                                              DSKVDPILIKCLAEKLEEQ
                                                                                                                                                                                                                                                        DVSDLQSKTRLVKWNYYEGFF-----YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKF
                                                                                                                                                                                                                                                                                FSGSAYFVVTREYVGYVLENENIQKLMEWAQDTYSPDEFLWATIQRIPEVPGSFPSSNKY
                                                                                                                                                                                                                                                                                            FVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDIYSPDEHFWATLIRVPGIPGEI-SRSAQ
                                                                                                                                                                                                                                                                                                                           IVRKLKCSTGENNLETEKMPPNKEERWK-----KRYAVVDGKL-TNTGIVKAPPPLKTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity 43.8
166; Conservative
 Bovinae;
           Eutheria;
                      Metazoa;
                                (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycosyltransferase; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĀĀ;
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428
58
95
49849
  Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32
9
                      Chordata;
           Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 1 %
                                                                                                                                                                                            421
                                                                                                                                                                                                                393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L(POTENTIAL).
L(POTENTIAL)
L(POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
F3FFD2517B27AAE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 837; DB 1;
Pred. No. 3.5e-54;
7; Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (I
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         II MEMBRANE PROTEIN.
ENZYME (IGNT).
                      Craniata; Vertebrata;
                                                                                                                                     427
             Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-anchor
             Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                   ,6-N-
2 BRANCHING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOLGI
                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          igh a collaboration EMBL outstation
             Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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                                                                    ENZYME)
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                                                                                                                                                                                                                                                                                                                                                                                             200
                                                                                                                                                                                                                                                                                                                                                                                                                     168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
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RESULT 4
BGIB_MOUSE
ID BGIB_M
AC P97402
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                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                        Dt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 170;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U41320; AAA83244.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
  BGIB_MOUSE
P97402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                   237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
                                                                                                                                                                                                                                 349
                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE II MEMBRANE PROSIMILARITY: TO I-BRANCHING ENZYME (IGNT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: GLYCOSYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNCSGIYEQEPLEIGK ---- SLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVSK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNI--SKEAPPHNIQIFVGSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEAGFPIAYSIVVHHKIEMLDRLLRAIYMPQNFYCIHVDAKSEKSFLAAAVGIASCFSNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNI 148
                                                                                                                                                                                  ILIKCLAEKLEEQ
                                                                                                                                                                                                                                 AIARFYKWQYFEGDYSKGAPYPPCS-VHVRSVCVFGAGDLNWLLHVHHLFANKFDTDIDL
                                                                                                                                                                                                                                                                             SKTRLVKWNYYEGFF----
                                                                                                                                                                                                                                                                                                                                                 FVLSQAFVKYIFNNSIVQDFFAWSKDIYSPDEHFWATLIRVPGIPGEISRSAQ-DVSDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                      MGENNLEGEKMPSHKKERWKKH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVASQLESVVYASWSRVQADLNCMQDLYQMNAGWKYLINLCGMDFPIKTNLEIVRKLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCTKILQGDVDEIQKVKLESLTVKFKKRARWTNYDYINMTGDCASFIKKRKYITEPLSK 116
                                                                                                                                                                                                                                                                                                                         FVVSREYVEYVLQNQNIQKFMEWAKDTYSPDEYLWATIQRIPEVPGSLSLSYKYDTSDMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 45.6 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33
52
58
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \begin{tabular}{ll} Glycosyltransferase; & Transmembrane; \\ Glycoprotein. \end{tabular}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
A
                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427
52
58
95
49733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.98;
                                                                                                                                                                                                                                                                          -YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LUMENAL, CATALYTIC (POTENT N-LINKED (GLCNAC. . .) (PO N-LINKED (GLCNAC. . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 831.5; I
Pred. No. 8.8e
54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (PO
SIGNAL-ANCHOR
(POTENTIAL).
                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      -YEVVNGKL-TNMGTDKIHPPLETPLFSGSAH
                          400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 1;
.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
DR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN. GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266
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                                                                                                                                                                                                                                                                               380
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γQ
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                                                                                                                            8
                                                                                                                                                       В
                                                                                                                                                                               QΥ
                     γ
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                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLCJUCOSAMINYLTRANSFERASE
(EC 2.4.1.150) (N-ACETYLGJUCOSAMINYLTRANSFERASE) (I-BRANCHING (IGNT) (LARGE I ANTIGEN-FORMING BETA-1,6-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLGLUCOSAMINYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Glycosyltransferase; Transmembrane; Golgi stack; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1100870; Gcnt2
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                        VINLCGODEPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTY-HHELRRVPYEYVKL
                                                HVDEKATAEFKGAVEQLVSCFPNVFLASKMEPVVVGGISRLQADLNCIKDLSTSEVPWKY
                                                               HYDRKAPDTFKVAMNNLAKCESNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKY
                                                                                                      MIHEKPSCTEYVTQSHYITAPLSQEEGDFPLAYVMVIHHNFDTFARLFRAIFMPQNIYCV
                                                                                                                                                         VCVVSYVLSFGGDQSYQKLNISDSVRLSQVCSSFID-----
AINTCGQDFPLKTNKEIVQYLKGLKGKNLTPGVLPPAHAIGRTRYVHREHLSKELSYV--
                                                                                                                               VVAMTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCI
                                                                                                                                                                                                             al Similarity
156; Conser
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Rodentia;
                                                                                                                                                                                                                         33.3%;
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                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                             (POTENTIAL).
LUMEDAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                            Score 730.5; DB 1;
Pred. No. 2e-46;
1; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                          -GKSRFLWRNKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                Signal-anchor;
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                                                                                                                                                                                                                                       Length 400;
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                                                                                                                                                                                                                23;
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RA MEDILINE-98070745; Pubmed=9405606;

RA Sasaki K., Kurata-Miura K., Ujita M., Angata K., Nakagawa S.,

RA Sasaki K., Kurata-Miura K., Ujita M., Angata K., Nakagawa S.,

RA Sekine S., Nishi T., Fukuda M.;

RA Sekine S., Nishi T., Fukuda M.;

RA Fression cloning of cDNA encoding a human beta-1,3-N-

RE Procession cloning of cDNA encoding a human beta-1,3-N-

RET acetyllactosamine synthesis.";

RE Proc. Natl. Acad. Sci. U.S.A. 94:14294-14299(1997).

RE Proc. Natl. Benauchical Sci. U.S.A. 94:14294-14299(1997).

RE Proc. Natl. Acad. Sci. U.S.A. 94:14294-14294(1997).

RE Proc. Natl. Acad. Sci. U.S.A. 94:14294-14294(1997).

RE Proc. Natl. Acad. Sci. U.S.A. 94:14294-14294(1997).

RE Proc. Natl. Acad. Sci. U.S.A. 94:1429
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
N-ACETYLLACTOSAMINIDE BETA-1.6-N-ACETYLGJUCOSAMINYLTRANSFERASE
(EC 2.4.1.150) (N-ACETYLGJUCOSAMINYLTRANSFERASE) (I-BRANCHING I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bierhuizen M.F.A., Maemura K., Kudo S., Fukuda M.; Genomic organization of core 2 and I branching beta-1,6-N-acetylglucosaminyltransferases. Implication for evolution obeta-1,6-N-acetylglucosaminyltransferase gene family."; Glycobiology 5:417-425(1995).
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Bierhuizen M.F.A., Mattei M.-G., Fukuda M.;
"Expression of the developmental I antigen by a cloned human cDN
encoding a member of a beta-1,6-N-acetylglucosaminyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
MEDLINE=96078409; PubMed=7579796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family
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                                                                             AND TO A LESSE
LIVER.
DEVELOPMENTAL
                                                                                                                                                          SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI.
TISSUE SPECIFICITY: IT THE ADULT, HIGHLY EXPRESSED IN PROSTATE AN
TO A LESSER EXYENT IN SMALL INTESTINE AND COLON. BARELY DETECTED
IN HEART, BRAIN, KIDKEY AND PANCREAS. NO EXPRESSION IN PLACENTA,
LUNG, LIVER, SKELETAL MUSCLE, SPLEEN, THYMUS, TESTIS, OVARY AND
PERIPHERAL BLOOD LEGUECOTYPES. IN FETUS, HIGHLY EXPRESSED IN BRAIN
AND TO A LESSER EXTENT IN LUNG AND KIDNEY. BARELY DETECTED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: GLYCOSYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R
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Metazoa; Chordata; C
Metazoa; Primates; (
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    AND ONCOGENESIS.
TO CORE 2 BRANCHING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -WTGNLRAVKWMDMEA-KHGGCQGHYVHGICIYGNGDLQWL
                                                                                     EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385
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                                                                                     INCREASES
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    (C2GNT).
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15-JUL-1998 ( 15-JUL-1998 ( 15-DEC-1998 ( HYPOTHETICAL

(Rel. 36, (Rel. 36, (Rel. 37, L PROTEIN M

, Last sequence update)
, Last annotation update)
MJ1054 (EC 1.1.1.-).

Archaea; Euryarchaeota; Methanococcus.

NCBI\_TaxID=2190;

Methanococcus

jannaschii

Methanococcales; Methanococcaceae;

Q58454;

METJA

STANDARD;

PRT;

895 8

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YA54_METJA
ID YA54_M
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Best Local
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EMBL; 219550; CAA79610.1;
EMBL; L1607; AAA99832.1;
EMBL; L41605; AAA99832.1;
EMBL; L41605; AAA99832.1; J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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600429; -.
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                                                                                                                                                                                                                         WFANKFDSKVDPILIKCLAEKLEEQQR
                                                                                                                                                                                                                                                  GVPGSMPNAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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314
388
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N-LINKED (GLCNAC...) (POTENTIL

N-LINKED (GLCNAC...) (POTENTIL

N-LINKED (GLCNAC...) (POTENTIL

N-LINKED (GLCNAC...) (POTENTIL

1469628690A1F43B CRC64;
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Pred. No. 5.3e-45;
3; Mismatches 129
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SIGNAL-ANCHOR (TYPE-II
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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(POTENTIAL)
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L outstation -
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Best Local S
Matches 91
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Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Godayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannashi.";
Science 273:1058-1073(1996).
Science 273:1058-1073(1996).
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SEQUENCE
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ACT_SITE
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TIGR; MJ1054; -.
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Pfam; PF00984; UDPG_MGDP_dh;
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719
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ween the Swiss Institute of Bioinformatics and the EMBL outst
Buropean Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                           EIDILE-ELSKTDLIEKVWIHNKDLATNEFNIIKPYLSNKYPHDVKRNGTIRAKDILPIK
                                                            SYKRNIEPLGYKKSDNFAILEVKEIIK-EHYSGYVYSVETENSL-LITSYGILIHNCEPK
                                                                                                                                                       FVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIP--
                                                                                                                                                                                                                    MLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFVGSAYFVLSQA
                                                                                                                                                                                                                                                      ENI - - LNCGINCYNKNIPPQMFNAKEEIKWEF -
                                                                                                                                                                                                                                                                                  AHISRLQADLNCLSDLL-----KSSIQWKYVINLCGQDFPLKSNFELVSELKKLNGAN
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DVKALIKQFENNNIEPILIKA-TDIVNEEQIKW
                              DGHWFANKFD-SKVDPILIKCLAEKLEEQQRDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
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895 AA;
                                                                                                                                                                                                                                                                                                                                               ------SNIFIASKLEAVEY
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                                                                                                                                                                                         -NLNIEFAT
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                                                                                                                            -----KST-----TMAYIIRINGLEQVKKIGELFGKKWENYKDIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 BY
102614 MW;
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20.1%; Pre
21.4ve 73;
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Pred. No. 0.52
73; Mismatches
                                                                                            -RIVKWNYYEGFFYPSCTGSHLRSVCIYGAAELRWLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAD (POTENTIAL).
BY SIMILARITY.
B511AA68CCA41445 CRC64;
                                                                                                                                                                                         ----VSKKM-AHSLLILLQLLGIVAS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994
01-FEB-1994
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                      DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jonniaux J.-L., Coster F., Purnelle B., Goffeau A.;
"A 21.7 kb DNA segment on the left arm of yeast chromosome XI
"A 21.7 kb DNA segment on the left arm of yeast chromosome XI
SSB1 and 8 new open reading frames of unknown function.";
Yeast 10:1639-1645(1994).
-!- FUNCTION: INVOLVED IN SIZE CONTROL; POSSIBLE RNA BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nash R.S., Futcher A. Submitted (AUG-1993)
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PROSITE; PS50102;
                                                                                                                                                                                                                                                                                                                                                              RNA-binding.
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                      283
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                                                                                                                        AINYAVILNSKNELFGPSFPNKTTVEIIDDTTKNLVSFPSSAIFNDTSRLNKSN--SGMK
                                                                                                                                                SIQWKYVIN----LCGQDFPLKSNFELVSELKK--
                                                                                                                                                                        KLSNVAKDITLRECYAIFALAEGYKSIELQKKNSSSSITSASLEDENDIFIIARFELLNL
                                                                                                                                                                                                                         RGSASGELYLNDTNSPLAISSMLNTLALGSMPQDIASSNISNH
                      PLSSQGQVIGLHSNHSHQDLSVESTIQTSDIGKSFLLRDNTEINEKIWGT---
                                              FVLSQAFVKY IFNNS IVQDFFAWS
                                                                      RPSILSQRSRFSFSDPFSNDSPLSQQQSQQQQQQQQQQQQQQHSTQKHSPQQCNQQQVNSSI
ISRSAQDVSDLQSKTRLVKW---
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661 A
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(Rel. 28, Last seq
(Rel. 34, Last ann
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02; RRM; 1.
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Pred. No. 1.
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 NYYEGFFYPSCTGS
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Mismatches
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                                              KDTYSPDEHFWATLIRVPGIPGE
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commercial
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Вb

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INGY --- MSTPQPSTPTLEWGNTSASQHGSSFFLPSAAST

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HSSP; P11362; IFGI.
InterPro; IPR00719; -.
InterPro; IPR001245; -.
InterPro; IPR003006; -.
Pfam; PF00047; ig; 2.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
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01-JUL-1993
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FIBROBLAST G
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Q01742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Seno M., Sasada R., Watanabe T., Ishimaru K., Igarashi
"Two cDNas encoding novel human FGF receptor.";
Biochim. Biophys. Acta 1089:244-246(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Receptor; Glycoprotein; Tyrosine-protein kinase;
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[3]
SEQUENCE FROM N.A.
MEDLINE=91274356; PubMed=1
Seno M., Sasada R., Watan/
ONAs encoding novel
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P21802; P18443;
01-NOV-1990 (Rel. 16, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR
(KERATINOCYTE GROWTH FACTOR RECEPTOR).
FGFR2 OR BEK OR BFR1 OR KSAM-1.
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TISSUE-Neonatal brain stem;
TISSUE-Neonatal brain stem;
MEDLINE=90360977; PubMed=1697263;
Dionne C.A., Crumley G.R., Bellot F., Kaplow J.M., Sear
Ruta M., Burgess W.H., Jaye M., Schlessinger J.;
"Cloning and expression of two distinct high-affinity r
cross-reacting with acidic and basic fibroblast growth
EMBO J. 9:2685-2692(1990).
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Eukaryota; Metazoa; (
Mammalia; Eutheria; E
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  TISSUE-Stomach cancer;
MEDLINE-90332706; PubMed-2377625;
Hattori Y. Odagiri H., Nakatani
Sakamoto H., Katoh O., Yoshida T.
                                                                                                                                                                                                                                                                                                      genome
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                                                                                                                                                                                                                                                                                                                    91045961; PubMed=2172978;
t E., Blanquet P.R., Champion-Arnaud
t E., Blantois Y., Breathnach R.;
a A., Courtois Y., Breathnach R.;
fibroblast growth factor receptor ge
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., Watchaabe T., Ishimaru K.,
ng novel human FGF receptor.
Acta 1089:244-246(1991).
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       , Nakatani H.
Yoshida T.,
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AND ARG-253.

AND ARG-253.

Let A.O.M., Slaney S.F., Oldridge M.,

Hockley A.D., Hayward R.D., David D.J.,

Malcolm S., Winter R.M., Reardon W.;

"Apert syndrome results from localized mutallelic with Crouzon syndrome.";

Nat. Genet. 9:165-172(1995).

[13]

VARIANTS PS PRO-341. **

(EDLINE=95235557*

Tilan**
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Steinberger D.
Submitted (APR
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95078932;
Reardon W., Winter
Malcolm S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel form of fibroblast growth factor splicing of the third immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93016048; PubMed=1400433; Dell K.R., Williams L.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugimura T., Terada "K-sam gene encodes tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "K-sam, an amplified gene in sheparin-binding growth factor Proc. Natl. Acad. Sci. U.S.A.
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MEDLINE=95384152; PubMed=7655462;
Oldridge M., Wilkie A.O.M., Slaney
Rutland P., Hockley A.D., Wake M.J.
Reardon W., Malcolm S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                         Lajeunie E.,
Renier D.;
                                                                                                                                                                                              MEDLINE=95235551;
                                                                                                                                                                                                                         "Mutations in the third immunoglobulin factor receptor-2 gene in Crouzon syndi Hum. Mol. Genet. 4:1077-1082(1995).
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. Chem. 267:21225-21229(1992)
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Y., Sasaki H.,
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r receptor genes.";
.. 87:5983-5987(1990)
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VARIANTS CS/JWS/PS.

X MEDLINE=96203627; PubMed=8644708;

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VARIANTS AS TRP-252 AND ARG-253.

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Tsai E.-J., Hwu W.-L., Lin S.-P., Chang J.-G., Wang T.-R., Tsai C.-

"Two common mutations 934C to G and 937C to G of fibroblast growth

"Two common mutations 934C to G and 937C to G of fibroblast growth

"Two common mutations 934C to G and 937C to G of fibroblast growth

"Two common mutations 934C to G and 937C to G of fibroblast growth
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MEDLINE=97114301;
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MEDLLNE=99180879; PubMed=9521881;
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VARIANTS
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Hayward R.,
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MEDLINE-98358420; PubMed-9693549;
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Hesseling-Janssen A.L., van den Ouweland A.M.
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Steinberger D., C
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MEDLINE=97295073; F
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656; PubMed=8946174;
Reardon W., Wilkes D., Rut
all C.M., Brueton L., Chun
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K., Howard T.D.,
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J. Craniofac. Surg. 9:207-209(1998).
-!- FUNCTION; RECEPTOR FOR ACIDIC AND BASIC
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01-MAY-1991 (Rel. 18, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR
(KERATINCYTE GROWTH FACTOR RECEPTOR).
FGFR2 OR ECT1 OR BEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                          TISSUE-Brain, and Liver;

MEDLINE-92228773; PubMed-1373495;

Mansukhani A., Dell'Era P., Moscatelli D.,

Hanafusa H., Basilico C.;
                                                                                  SEQUENCE FROM N.A
MEDLINE=91095977;
                                                                                                                                                                                                "Characterization of the murine receptor: activation by three me requirement for heparin.";
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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MANDIBULAR PROGRATHISM.

MANDIBULAR PROGRATHISM.

MANDIBULAR PROGRATHISM.
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Acad. Sci.
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cloning
                                                     T.P.,
                                               . (SHORT FORM).
PubMed=1846048;
T.P., Bottaro D.P.,
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Pred. No. 4.5;
35; Mismatches
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EMBL; M86441; AAA37286.1; -.
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EMBL, M63362; AAA39377.1; -.
EMBL, M63362; AAA39385.1; -.
PIR; A31378; TVMSBK.
PIR; A38429; A38429.
HSSP, PI1362; 1FGI
MGD; MGI:95523; FGfI2.
InterPro; IPR000719; -.
InterPro; IPR001245; -.
InterPro; IPR001245; -.
Pfam; PF000647; i; 3
Pfam; PF000647; i; 3
Pfam; PF00069; TYRKINASE.
PRINTS; PR00109; TYRKINASE.
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"Novel tyrosine kinase identified by phosphotyrosine antibody
"screening of cDNA libraries.";

Mol. Cell. Biol. 8:5541-5544(1988).

-i- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.

-i- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.

POSSESSES A HIGHER AFFINITY FOR ADDICTHAN FOR BASIC FGF'S.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN (A LONG AND A SHORT FORM) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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Science 251:72-75(1991).
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Transferase; Phosphorylation; Transmembrane; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00107; PROTEIN_KINASE_ATP;
PS00109; PROTEIN_KINASE_TYR;
PS50011; PROTEIN_KINASE_DOM;
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                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                    PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                    (BY SIMILARITY).
   (HZ
                 GLCNAC.
                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                      GROWTH
   SHORT
                                                                                                                                                                                                                                                                                                                                                                                  OWTH FACTOR (POTENTIAL)
   ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding;
                (POTENTIAL)
                                                                                                                                                                                                                    (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL
                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
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SOFFIFF

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Query Match
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Matches 78
                                                                                                                                                                                                                                                              068007;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BACITRACIN SYNTHEMASE 2 (BA2) [INCLUDES: AFP-DEPENDENT LYSINE
ADENYLASE (LYSA) (LYSINE ACTIVASE); AFP-DEPENDENT D-CRNITHINE
ADENYLASE (D-ORNA) (D-ORNITHINE ACTIVASE); ORNITHINE RACEMASE
(BC 5.1.1.12)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
VARSPLIC
                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-AFCC 10716;
MEDLINE-98089193; PubMed-9427658;
KONZ D., Klens A., Schoergendorfer K., Marahiel M.A.;
KONZ D., Klens A., Schoergendorfer Marahiel M.A.;
"The bacitracin biosynthesis operon of Bacillus licheniformis
"The bacitracin biosynthesis operon of three multi-modular pepti
                                                                                                                                                                                                                                                                                                                                                                                                   BACLI
                                                                      -i- FUNCTION: ACTIVATES TWO AMINO ACIDS AND INCORPORATE FROM ITS SECOND ACTIVE SITE INTO BACITRACIN.
-i- CATALYTIC ACTIVITY: 1.-CORVITHINE - D-ORNITHINE.
-i- COPACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETH
                                                                                                                                                                                                                                                     Bacillus licheniformis.
Bacteria; Firmicutes; F
                                                                                                                                                                                                                                                                                                                                                                                       BACB_BACLI
                                                                                                                                synthetases."
                                                                                                                                                                                                                             NCBI_TaxID=1402
                                                                                                                                                                                                                                          Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
  PATHWAY: NON-RIBOSOMAL BIOSYNTHESIS OF THE CYCLIC PEPTIDE ANTIBIOTIC BACIFRACIN.
SUBUNIT: LARGE MULTIENZYME COMPLEX OF BA1, BA2 AND BA3.
DOMAIN: CONSISTS OF TWO MODULES WITH A C-TERMINAL EPIMERI DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID INTO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFGQVVMAEAVGIDKDKPKEAVTVA-VKMLKDDATEKDLSDLVSEMEMMKMIGKHKNIIN
                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYYKKTTNGRLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L----CGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAVPSQRPTFKQLVEDLDRILTLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLPSEK-LF----MDRNLTTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLMWEIFTLGGSPYPGIPVEELFKLLKEGH----RMDKPTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEHFWATLIRVPGIPGEISRSAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRTNISKEAPPHNIQIFVGSAYFV-----LSQAFVKYIFNNSIVQDFFAWSKDTYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLGACTQDGPL---YVIVEYASKGNLREYLRARRPPGME-----YSYDINRVPEEQMTF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity 24.(78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169
187
821
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                                                                                                                       4:927-937(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;
                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EAVEYAHISRLQADL--NCLSDL-----LKSSIQWKYVIN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
187
91983
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361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AAELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQQRD-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.7%;
                                                                                                                                                                                                                                           Bacillus/Clostridium us group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN SHORT ISOFORM).

AAGVUNTTDKEIEVLYIRNVTFEDAGEYTCLAGNSIGISFHS
AMUTVLT -> HEGINSSNAEVLALFUNTEMDAGEYICKVS
NYIQQANGSAMLTVLFKQQ (IN SHORT ISOFORM).

C -> V (IN REF. 2).

S -> P (IN REF. 2).
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCDB28ADD61F4414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102.5;
No. 4.
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                                                                          PHOSPHOPANTETHEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                       group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
                                                   CYCLIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTNE-LYMMMRDCW
                EPIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -HQSDVWSFG
                                                                                                            A D-ORNITHINE
                                                                                                                                              ormis ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103;
     PEPTIDE
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BINDING
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                PROSITE; PS00012; PHOSPHOPANTETHEINE; PROSITE; PS00455; AMP_BINDING; 2. PROSITE; PS50075; ACP_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000255; -.
Interpro; IPR000873; -.
Interpro; IPR001242; -.
Pfam; PF00501; AMP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF007865; AAC06347.1; -.
                                                                                                                                                                                                                                                                                                                                             Pfam; PF00550;
                                                                                    DOMAIN
                                                                                                          DOMAIN
                                                                                                                                   REPEAT
                                                                                                                                                                                      Multifunctional
                                                                                                                                                                                                            Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANGUES: BACTTRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC DODECAPEPTIDES, THAT DIFFER BY ONE OR TWO AMINO ACIDS. THE MOST ABUNDANT IS BACITRACIN A, A BRANCHED CYCLIC DODECAPEPTIDE. IT CONTAINS AN N-TERMINAL LINEAR PENTAPEPTIDE MOIETY (ILE-CYS-LEU-D-GLU-ILE) WITH AN ISOLEUCINE-CYSTEINE THIAZOLINE CONDENSATION PRODUCT AND A C-TERMINAL HEPTAPEPTIDE RING (LYS-D-ORN-ILE-D-PHE-HIS-D-ASP-ASN), IN WHICH THE FREE ALPHA-CARBOXY GROUP OF THE CTERMINAL ASN IS BOUND TO THE EPSILON-AMINO GROUP OF LYSINE. IT CONTAINS FOUR AMINO ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHE-9, AND ASP-11).
SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHYLATION (OPTIONAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBSTRATE ADENYLATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INITIATION MODULE), AND EPIMERIZATION (OPTIONAL),
                                                                                                                                                                                                                                                                                                                    PF00668; DUF4; 3.
PF00550; pp-binding; 2
s; PR00154; AMPBINDING
                                                                                                                                                                                                               Isomerase; Antibiotic biosynthesis; Phosphopantetheine;
                            1547
1021
1021
2064
1051
2094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE TE ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE
                         l enzyme;
1090
5 1090
7 2141
7 1037
1 1037
4 2104
4 2094
     AA;
        297474 MW;
                                                                                                                                                                                      Repeat.
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                                                                                                                                      DOMAIN 1
DOMAIN 2
     PHOSPHOPANTETHEINE (I PHOSPHOPANTETHEINE (I PHOSPHOPANTETHEINE (I PHOSPHOPANTETHEINE (I PHOSPHOPANTETHEINE)
                                                                              DOMAIN 2 (D-ORNITH ACYL CARRIER (ACP) ACYL CARRIER (ACP)
                                                                                                                                   (LYSINE-ACTIVATING).
(D-ORNITHINE-ACTIVATING)
                                 (BY SIMILARITY)
        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
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Query Match
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Matches 85
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               286
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                                            782
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                                                                                                                                 181
                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                            KDEVRYEVNCSG---IYEQEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYA
                                                                                                                                                                                                                                                                                 EDRVKYMLEDSGADMVVIQEPFK----SKIDGRQLITAED-----TRSFS
FFAWSKDTYSPDEHFWATLIRVPGIPGEISRSAQDVSD--LQSKTRLVKWNYYEGFFYPS: | | | | | | | | | | | | | |
                                                                                                                             QWKYVINLCGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRV----
                                                                                                                                                                                                                                                   QKLVSKEEKSFPIAYSLVVH-----KDAIMVER-LIHAIYNQHNIYCIHYDRKAP----
                                            VLKFEYVE---
                                                                       --PYEYVKLPIRTNISKEAPPHN----IQIFVGSAYFVLSQAFVKYIFNNSI-----VQD
                                                                                                      KYRVTLVSCS---PL----LLNEI--
                                                                                                                                                              DTVLQVVSFSFDAFSEEVYPILACSGRLVISRKV--
                                                                                                                                                                                                                          KENLPNVNKASDLAYVIYTSGSSGRPKGVMTTHRNVVH
                                                                                                                                                                                                                                                                                                                                          Similarity 19.85; Conservative
                                                                                                                                                                                            DTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSI
                                          - NIIKGADVYNSYGPTEATVCATYYQLSSADRK---KTSIPIGKPLSN
                                                                                                                                                                                                                                                                                                                                                       4.6%;
                                                                                                                                                                                                                                                                                                                                         Score 100.5;
Pred. No. 29;
71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                            128;
                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                        DKNQHLTFHPQMKFISGGD
                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                               -SDLN-IDELVKTIG
                                                                                                                                                                                                                            YVDAFTKRIPLSEH
                                                                                                                                                                                                                                                                                                                                                                          2607;
                                                                                                                                                                                                                                                                                                                                               145;
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                   745
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                                                                                                                                                                                                                                                        131
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                 343
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                                                                                                        781
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RESULT
VO01_VP
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Best Local
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01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91021027; Pul
Goebel S.J., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      Paoletti E.;
Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VOO1_VACCC
                                                                                                                                                                                                                                                                                  EMBL; M35027; AAA48053.1;
PIR; D42510; D42510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete DNA sequence of Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 880
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506
                   191
                                          456
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                                                                                     404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGSHLRSVCIYGAAEL-RWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQQRDWITLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKVYIADQYGRPQPV--
                                                                                    KIV-KDWKSCALTLSAI---KGIMVTDTINTVLSK----ILHHHRNVFKYLTSVENKEIA
                                                                                                                              KDTDSLEDILAHIDNARKNSKYSIEDVERIISSFRLNPCVVRRTMLSDIDIKTKI--MVL
                                                                                                                                                    RDIIDLED----
                                                                                                                                                                        VEVNISYYDF --- RYRQFADEFRDYIM --- IKERRQITMQSGDRIRRFRRPMSLRSTIIK
                                                                                                                                                                                              VEYSLSTSPFVRNRYTHVKDEVRYEVNCSGIYEQEPLEIGKSLEIRR------
                   QDF--PLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTN
                                                               MNNLAKCFSNIFIASKLEAVEYAHISRLQADLNC-----LSDLLKSSIQWKYVINLCG
                                                                                                       KLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRK-----APDTFKVA
QRCWGPLTEMLFNENKKKKLN-
                                          VCNCSRCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u></u>2
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                         666
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(Rel. 17, Last seq
(Rel. 17, Last ann
                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pubMed=2219722;
son G.P., Perkus
                                                                                                                                                                                                                                                                     7,7577 MW;
                                                                                                                                                                                                                            4.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
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                                            ·LFYRELKSVRCDLRTDDGLLDRLYDLTRYALHGKINQNLIG
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                                                                                                                                                                                                                                                                                                                                                                                                                             Perkus M.E.,
                                                                                                                                                                                                                    50;
                                                                                                                                                    ---DDVV----
                                                                                                                                                                                                                  Score 99.5; D
Pred. No. 5.7;
50; Mismatches
 -NLMEYIKIS----DMLVYGHSI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccinia
                                                                                                                                                                                                                                                                         46DF3299DDEB66EF CRC64;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation (EC 2.
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HSSP; P11362; 1FGI.
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   -VLNDQYAKIVIFFNTIIEYIIA
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R HSSP; P11362; Lrv...

R HSSP; P11362; Lrv...

R InterPro; IPR000719; ...

PR InterPro; IPR001245; ...

PR InterPro; IPR001245; ...

DR InterPro; IPR001006; ...

DR Pfam; PF00047; ig; 3.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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SEQUENCE FROM N.A.
MEDIJIND-87053814; PubMed-3536478;
Eisel U., Jarausch W., Goretzki K., H.
Weller U., Hudel M., Habermann E., Ni.
"Tetanus toxin: primary structure, ex
homology with bottlinum toxins.";
EMBO J. 5:2495-2502(1986).
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13-AUG-1987 (Rel. 05, Las
13-AUG-1999 (Rel. 38, Las
15-JUL-1999 (Rel. 38, Las
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                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium
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  SEQUENCE OF 742-1314 FROM N.A. MEDLINE=86085672; PubMed=3510187; MEDITMEEN N.F., Lyness V.A., Pickard "Cloning, nucleotide sequencing, and ex
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PARTER REPORTED FOR THE PROPERTY OF THE PROPER

EMBL; X04436; CAA28033.1; EMBL; M12739; AAA23282.1; EMBL; X06214; CAA29564.1;

restrictions

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fragment C in
J. Bacteriol.
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MEDLINE=92037649;
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"Arrangement of disulfide bridges and
in tetanus toxin.";
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Nat. Struct. Biol. 4:788-792(1997).

1-:- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMI RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS I AND MOVES BY RETROGRADE TRANSPORT UP THE AKON INTO THE WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPERTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dasgupta B.R., Montecucco C.;
"Tetanus and botulinum-B neurotoxins block
by proteolytic cleavage of synaptobrevin.";
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neurotransmitter release an
EMBO J. 11:3577-3583(1992).
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Nature 359:832-835(1992).
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MEDLINE=93063293; PubMed=1331807;
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isbsorsend an email to license@isb-sib.ch).
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MEDLINE=97475217; PubMed=9334741;
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165:21-27(1986).
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InterPro; IPR000395; -.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
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      (Rel. 32, Created)
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L 244.6 KDA PROTEIN (ORF 2054).
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Proc. Natl Acad. Sci. U.S.A. 91:9794-9798(1994).
-:- FUNCTION: NOT YET KNOWN.
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Pfam; PF00004; AAA; 1.
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Sugiura M.;
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T., Tsudzuki J., Ito S.,
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L outstation -
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                                                              1094
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	1 49.5 2 71.5 3 321.5 4 313.5 5 29.6 6 29.6 7 288.5 9 245.5 11 218.5 12 218.5 14 196.5 196.5	and is de	Database :  Pred. No.	Minimum DB seq 1 Maximum DB seq 1 Post-processing:	Searched: Total number of	Scoring table:	Title: Perfect score: Sequence:	Run on:	OM protein - pro
5 447 2 T00966 447 2 T00966 3 513 2 T20068 3 67 2 T218892 1 467 2 T218892 1 466 2 F96571 3 95 2 F96571 6 394 2 T51450 6 30 2 T02524 0 384 2 T08940 0 398 2 T08940 0 371 2 T21819 6 371 2 T21819 6 371 2 T21819 6 6 1 2 S50734	426 2 A462297 400 2 A462297 445 2 T21262 425 2 T20207 401 2 T24929 454 2 T21261 472 2 T24930 459 2 T24742 470 2 T32138 489 2 T32434 486 2 T32434	by analysis of the total score distribution.  SUMMARIES  Length DB ID  Descrip	pir_68 *  1: pirl:*  2: pir2:*  4: pir4:*  4: pir4:*  No. is the number of results predicted by chance to have the table to the pirate.	Length: 0  ength: 2000000000  Minimum Match 0%  Maximum Match 100%  Listing first 45 summaries	219241 segs, 76174552 residues hits satisfying chosen parameters: 219241	BLOSUM62 Gapop 10.0 , Gapext 0.5	US-09-645-192-2_COPY_39_453 2194 1 POKDIYLVEYSLSTSPFVRNDWITLPSEKLFMDRNLTTTS	August 2, 2001, 14:45:50 ; Search time 25.93 Second (without alignments) 1219.145 Million cell u	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. protein search, using sw model
al prote conditions al prote conditions al prote by 6-dehyd al prote by 6-dehyd al prote by 6-dehyd al prote by 6-dehyd by 338	prote Db 14 prote Oy 47 prote Oy 47 prote Db 71 prote Db 71 prote Oy 101 prote Db 129 prote Db 129 prote Db 129 prote Db 129 prote Db 189	C; Keywords C; Keywords Ouery Mat On Best Locc Matches	A; Title: A; Refere A; Recess A; Status A; Molecu A; Residu A; Cross A; Experi	A46033 A46033 beta-1,3-galact C.species: Hom C.pate: 20-Oct- C.pate: 20-oct- C.pate: non- Accession: A4 R;Bierhuizen, N Proc. Natl. Acc	TITORED TO THE TITORE	. 10	41 10 41 10 42 10 43 10 44 10	s 37 10 38 10 9dates/sec 39 10 40 10	
NSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFVG:	POKDIYLV-EYSLSTSPFVRNRYTHVKDEVRY	s: glycosyltransferase; hexosyltransferase; tra latch 38.7%; Score 849.5; DB 2; I cal Similarity 43.0%; Pred. No. 1.1e-56; 181; Conservative 70; Mismatches 129; I	ber: A4629; MUID:93028457 16293 1629	-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-a s: Homo sapiens (man) 20-Oct-1993 #sequence_revision 18-Nov-1994 #text ion: A46293 izen, M.F.; Fukuda, M. tl. Acad. Sci. U.S.A. 89, 9326-9330, 1992 tl. Acad. Sci. U.S.A. 89, 9326-9330, 1992	ALLIGNMENT'S	.5 4.6 437 2 T23	.5 4.7 821 1 .5 4.7 821 1 .5 4.7 821 1 .5 4.7 822 2 .5 4.7 822 2	4.7 707 2 4.7 707 2 4.7 769 2 4.7 820 2	00.00 00.00 00.00 00.00 00.00

100.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	103.5	104	104	104	106.5	108
4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.9	4.9
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aipna-1,3-mannosyi	tibroblast growth	. 4			C		ct	fibroblast growth	heparin-binding ii	hypothetical prote	probable membrane	serine/threonine-s	hypothetical prote	BTB domain and Ank	hypothetical prote

SKVDPILIKCLAEKLEE 392 || |:|| | | /DVDLFAIQCLDEHLRH 420 GSAYFVLSQAFVKYIF 278 CLVSKEEKSFPIAYSLV 100 ::||| |||||:| ::|| | 1100 )LKKLNGANMLETVKPP 220 || | | | || | | |KLLMGENNLETERMP 248 FSNIFIASKLEAVEYA 160 919.1; PID:g183441 xt\_change 21-Jul-2000 15900, NCBIP:115901) NAC:Gal beta 1-3-GalNAC-R (GlcN -acetylglucosaminyltransferase Length 428; Indels 41; Gaps 11;

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R; Wilkinson, J.
submitted to the EMBL Data Library,
A; Reference number: 219397
A; Accession: T21262
                  A;Gene: CESP:F22I
A;Map position: 1
A;Introns: 65/3;
                                                                                     A:Status: preliminary; translated from GB/EMBL/DDB
A;Molecule type: DNA
A;Residues: 1-445 <WIL>
A;Cross-references: EMBL:271262; PIDN:CAA95817.1;
A;Experimental source: clone F22D6
                                                                                                                                                                                                                                                           hypothetical protein F22D6.11 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bierhuizen, M.F.; Mattei, M.G.; Fukuda, M. Genes Dev. 7, 468-478, 1993
A;Title: Expression of the developmental I antigen A;Reference number: A46297; MUID:93194065
A;Accession: A46297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: nucleic acid
A; Residues: 1-400 <BIE>
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994
C;Accession: A46297
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Matches 143
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                                                       CESP: F22D6.11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVPGSMPNAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIPGEISRSAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYGAAELRWLIKDGH 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALKPPPPHNLTIYFGSAYVALSREFANFVLHDPRAVDLLQWSKDTFSPDEHFWVTLNRIP
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                    95/2; 136/3; 180/3; 256/3; 281/3; 403/3
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Pred. No. 2.9e-46;
3; Mismatches 129;
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                                                                                                      GSPDB:GN00019; CESP:F22D6
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A; Molecule type: DNA
A; Residues: 1-425 <WI2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C54C8.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15.Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T20207; T27478 R;Dobson, R.
                                                                                                                                                                                                                        A; Introns: 29/2; 117/3; 161/3; 195/3; 237/3; 266/3; 295/1; 313/3; 355/1; 374/2
                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: AL032664; PIDN: CAA21769.1;
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A;Experimental source: clone C54C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-425 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z19237
                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                                  A; Gene: CESP: C54C8.11
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                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLI---RVPGIPGEISRSAQ 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QILKHLNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEEKSFPIAYSLVVHKD--AIMVER---LIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DINCLNIFNGSKNRNQLRIVNSRSI-----EDKLLYSTDRCQTLKSLFRFNKVPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISYKNNYETNLTYPTDGWRYYISRDQIWSKPNCHNYMKAGSCYFGIGDYPRLLKSKALVA
                                                                                                                      1 Similarity 23.2 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99;
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TSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIY 116
                                                                                                                                       14.3%;
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                                                                                                                        80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN: CAB05469.1; GSPDB: GN00019; CESP: C54C8.11
                                                                                                                   Score 313.5; DB 2;
Pred. No. 3.7e-16;
D; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 321.5; DI
Pred. No. 9.8e-
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                                       -CQKMFDGDPVSLA-----RGALFKFDDRE
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                                                                                                                   Indels
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A; Introns: 45/3; 75/2;
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A; Residues: 1-401 <WIL)
A; Cross-references: EMBL: 283125; P
A; Experimental source: clone T15D6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z19956 A; Accession: T24929 A; Status: preliminary; translated f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T15D6.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC;Accession: T24929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQK 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRYQQYVNRAPVKCKGYYYRLSCVFGVYDLPNLINRHELVAHKLYFSYQPAAFMCLVENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPDEHFWATLIRVPGI------PGEISRSAQDVSDL-QSKTRLVKW------NYYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVPYEYVKLPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLKSSIQWKYVINLCGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELR 234
                                                                                                                                                                                                                                                                                                   THVKDEVRYEVNCSGIYEQEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LPFEFYRLNRKRPWSSPLPLYKTSL---SATF--SRKSANFMVNSEKVLEQIDFLRGTT
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                                                                                                                                                                                                                                   QKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLA 142
                                                                                                                                                                                                                                                                   TDLLDDL -- EINCINIL -- QGLKNEKQLELINIKMI -- - EDKLWNSIDRCHIVKSMFREN
SSLSSLIPRKAANYLASSSIPQQLLEFLRNTWVADEGFWGTLFGNKGLFDVPGSLN----
                              GSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPG---IPGEISRSAQ 319
                                                                                                  SELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFV 262
                                                                                                                                  DCFPN-----KRPPITWGSYEIINSVYDCLKFLSHLKSNWKYFQYLSGVDIPLKTNLEMV
                                                                                                                                                                  KCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELV 202
                                                                                                                                                                                                  EVPLSEEEARFPLSYGLLVYKELSQVLFMLSSIYQPQNEYCIAVGENSASTFLILLEELS
                                                                                                                                                                                                                                                                                                                                     86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    111/3; 151/3; 227/3; 252/3;
                                                                                                                                                                                                                                                                                                                                                   13.5%;
                                                                                                                                                                                                                                                                                                                                   ; Score 296; DB 2; I; Pred. No. 7.2e-15; 68; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAB05620.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                       296/2;
                                                                                                                                                                                                                                                                                                                                                                   Length 401;
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                                                                   LGQNETESPLPLFK
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hypothetical protein F22D6.12 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T21261 R;Wilkinson, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data A; Reference number: Z19397 A; Accession: T21261
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A; Map position:
A; Introns: 62/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-454 <WIL>
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                                                 hypothetical protein F44F4.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C;Accession: T22188 R;Coles, L.
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submitted to the EMBL Data A; Reference number: Z19528 A; Accession: T22188
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                                                                                                                                                                                                                                                                                                                                                                                                                     SHLETDWRYFQYLSGVDIPLKTNLEMVQILKHLNGTSNVEIT---NYQQARLTGKNE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLKTLERENTNPMSAEEKHEPLSYGMLVYKDLPQVTPARMEIKLHELEINLQVLFLLSSI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLKSICTTASDSYLLDNMEINCSNIL--KGYKTNEKLDIMHLDII---EEQLFSCTNKCQ 94
                                                                                                                                                                                                             NYMKDDSCVFGIGDVPRLRTSKALVAHKFYLKSEPEAYFCL---LKEHHR
                                                                                                                                                                                                                                          SHLR-SVCIYGAAELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQQR 395
                                                                                                                                                                                                                                                                              ADEGFWGTLFGNKDQFNISGSINSKDWMEYRDNQNNIFNPTDGWSYYISRDQIWDPELCK
                                                                                                                                                                                                                                                                                                                                                                                VPYEYVKLPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKSSIQWKYVINLCGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHPQNEYCIAVGENSAPIFQNLLREVSTCFSNVHF-MKRPPISWGSHEIIDSVYDCLEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDL
                                                                                                                                                                                                                                                                                                               PDEHFWATLIRVP----GIPGEI-SRSAQDVSDLQSK--TRLVKWNYY----EGFFYPSCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , 92/2; 190/3; 266/3;
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                                                                                                                                                                                                                                                                                                                                                ----NESP---LPLFKSSLSAIIPRKAANQLASSNTARKLLEFLWNTEI
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                                   Library, September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 291; DB 2
Pred. No. 2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291/3;
                                                                                      15-Oct-1999 #text_change 15-Oct-1999
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A;Status: preliminary; translated from GB/EMBL/DDB
A;Molecule type: DNA
A;Residues: 1-472 <WIL'>
A;Cross-references: EMBL:237092; PIDN:CAA85457.1;
A;Experimental source: clone F44F4
C;Genetics:
A;Gene: CESP:F44F4.6
A;Map position: 2
A;Introns: 57/2; 105/2; 185/3; 261/3; 319/1; 370/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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                                                                                                                                                                                                                                    R;Dobson, R.
submitted to the EMBL Data
A;Reference number: Z19956
A;Accession: T24930
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В
                     QY
                                                                                                                   A; Map position: A; Introns: 55/3;
                                                                                                                                                                                                                                                                                                       hypothetical protein T15D6.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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Best Local
                                                                                                                                                                                                                                                                                             Accession: T24930;
                                                                                                                                                             Genetics
                                                    Matches
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  44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEAEYPLAYGLVYYKTIVQVLTQMSLFYQPQHMFCITVDDQSPNEYKSVIQALPSCFPNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSN- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVVPREGADYLISSPRVQKLLKYLSKTWIPDESFWSTVLGSPALLPVPGSI--RVRDILW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFVGSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HVFIG---EPSQWGSFGILKNYYTCFNWLSKSKQKWKYYQYLSGTDLPIRTNLEMVRIFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENIPLECNSVINGTENRRKISRARQWDWHFDWVEHEIFNSRNVCSTIDKYFNFTRIPSSR
                                                                                                                                                                                                                                                                                                                                                                                                                               FANKFDSKVDPILIKCLAEKLEEQQ------RDWITLPSEKLFMDRNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPG---IPGEISRSAQDVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -IFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELK
                         THVKDEVRYEVNCSGIYEQEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYA
                                                                                                                                                                                                                                                                                                                                                                                                      VAHKLYLEFQPAAFMCMLKEVRRRSLSPDAHLFSARSYSQMPTVELYQGKAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRKNFKLRPPYENTVNSIGTSYIGRYQVWGWQKECFGKVKDFSCVFGVEDIEEIMTRPEL
 TDLLDDL--QINCTNILQGFKNE--NTLELINTKMI---ENKMWNSTDRCQTLTSMFRFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91;
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                                                                 Similarity
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                                                                                                                     85/2;
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VKWNYYEGF----FYPSCTGSHLRSVCIYGAAELRWLIKDGHW
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                                                                                                                     121/3; 161/3; 237/3;
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                                                                 12.1%;
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                                                      64;
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Pred.
                                                  Score 265; DB 2;
Pred. No. 1.6e-12;
4; Mismatches 157;
                                                                                                                                                                                                                                                                    November
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No. 3.3e-14;
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                                                                             Length 402;
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                                                      Indels
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                                                      62;
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Best Local S
Matches 106
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A;Status; PACALERA, MOIecule type; DNA
A;Residues: 1459 <WIL>
A;Cross-references: EMBL:Z81147; PIDN:CAB03536.1;
A;Cross-references: cione T09E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;McLay, K.
submitted to the EMBL Data
A;Reference number: Z19930
A;Accession: T24742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T09E11.9 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C:Accession: T24742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1
A; Introns: 39/1; 78/3; 204/1;
C; Superfamily: Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESP:T09E11.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWAT-----LIRVPGIPGEISR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCFPN-----KRPPIKWGSFEIINSVYGCLEFLSHLKSDWKYFQYLSGVDIPLKTNLEMV
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IFVGSAYFVLSQAFVKYIFNNSIVQDEF-AWSKDTYSPDEHFWATL--IRVPGIPGEISR 316 | :| | :| | :| | :||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHKLYIESEPEAFFCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                        VYYLMFS-SKSLFGRN-
                                                                    ELEQVYEWLGGANDVELL-PEAQRLDEENFKWD----PRSLKMFPDESKVDETILNEKIK
                                                                                                                ELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQ 259
                                                                                                                                                              AMAACLPNVLLLPDQEPIDSNGHNVNLAHLNCLRALINKP-GWNYAMLLQNHDLLTKSVY
                                                                                                                                                                                                     NLAKOFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNF 199
                                                                                                                                                                                                                                                   RIIPHDHILRPLKNGVAFARIVYKDYELVEKQVQMSYHPQNSFCFAIDKKAPTRFKNQMR 190
                                                                                                                                                                                                                                                                                                                                           KIEHFYSKTYRRRSETAHVDCGRILSGDKDYLQTVSG--ENRIPMVENPNPDMSCSAVMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity 22.
106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            -----DDVVAMTSDCDIYQTLRGYAQKLVSKEEKSFP------
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22.8%; pre
74;
                                                                                                                                                                                                                                                                                   IAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMN 139
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s elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 245; DB 2;
Pred. No. 6.2e-11
4; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338/3; 371/3;
s hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                        EQNSYALYNLRNENYQREAIINELRRDFAKIES 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RS-CVFGIGDVPNLMKSRALV
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protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LNGKNKTESP---LPLFK
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A;Map position: 1
A;Introns: 80/3; 191/1; 278/1; 325/3; 365/2; 407/3
C;Superfamily: Caenorhabditis elegans hypothetical protein H41C03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T27F6.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000 C;Accession: T25382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
hypothetical protein R07C3.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Apate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tc; Accession: T32137 R; Lamar, B.; Kramer, J. Submitted to the EMBL Data Library, July 1997 A; Description: The sequence of C. elegans cosmid R07C3 A; Reference number: Z21125 A; Accession: T32137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:282060; P
A;Experimental source: clone T27F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-454 <WIL>
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Best Local Similarity
Matches 80; Conserv
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                                                                                                                                                                                               1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLR-SVCIYGAAELRWLIKDGHWFANKFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                           KEAP---PHNIQIFYGSAYFYLSQAFYKYIFNNSIVQDFF-AWSKDTYSPDEHFWAT--L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMASCLPNVLLLPGRFFKNPIHDLSVDSHGHNTNL-AHYNCLRALINKP-GWNYAILLQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HDLITKSVYELEKIFNWLGGANDV-AIRPELGRLDK----KHFKWDPMSLKLFRNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLAKCFSNIFI------ASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCG 190
                                                                                                                                                                                                                                                     MAKSEHLMFNKVLPLFDYSIIECTAELL 424
                                                                                                                                                                                                                                                                                   LIKDGHWFANKFDSKVDPILIKCLAEKL 390
                                                                                                                                                                                                                                                                                                                                SDFLGMPGHFTDKCIKKGIITEGITRFAQWTHGD.
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Pred. No. 1.7e-09
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                                            cosmid R07C3
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                                                                                                                      #text_change
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Atholecule type: DNA A;Atholecule type: DNA A;Atholecule type: A;Cross-references: EMBL:AF016686; PIDN:AAB66233.1; GSPDB:GN00020; CESP:R07C3.A;Experimental source: strain Bristol N2; clone R07C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 2
A;Introns: 18/1; 78/3; 189/1; 276/1; 319/3; 359/2; 401/3; 441/3
C;Superfamily: Caenorhabditis elegans hypothetical protein H41C03.3
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                                                                                                                                                                                 A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-489 <WIL>
                                                                                                                                                                                                                                                       submitted to the EMBL Data A; Reference number: Z19830
                                                                                                                                                                                                                                                                                                         hypothetical protein R07B7.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc;Accession: T24013
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                                                                               A; Map position: 5
A; Introns: 42/3;
                                                                                              A; Gene: CESP: R07B7.6
A; Map position: 5
                                                                                                                                                                                                                                                                                            R; Harris
                                                                                                                                                   A; Experimental source:
                                                                                                                                                                      A;Cross-references:
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Best Local s
Matches 90
                                                                                                                                   Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATLIRVPGI--PGEISRSA-QDVSDLQSKTRLVKW-NYYEGFFYPSCTGSHLRSVCIYGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFF-AWSKDTYSPDEHFW 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYLMLLQNHDVITKSVYELDRIFELLGGVN-----DVFMSREIPERRKKHLKWDLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYVINLCGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIHYDRKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTSDCDIYQTLRGYAQKLVSKEEKSFPI----AYSLVVHKDAIMVERLIHAIYNQHNIY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKRITEALRTVDRSCEEQGFYCKRPETQHVDCGRVLVGDKIQLRAFQVYLQSLTGSNRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDFRAI - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AELRWLIKDGHWFANKFDSKVDPIL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STFQMSPDLKMPGHFTNECIHNDTAIVTISRLARWVPIYLDRAAHCATGTVRHDICIFGI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKLFRNDSKNS-DYELEISSGSVHSSLSRAAVKWLVEEVDLSIFIDQWNQTDYGADEQFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFAIDANSSAEFQRKMKKLEQCLPNVVVLPVTESYDSKGHNINLAHYNCMKK-LESLRGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIENSFLNLTCSAIKSRIIPKTAQFKPLKLNGTAFARIVFADYEFIEKQVQASYHPQNVF
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90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
                                                                                   80/2;
                                                                                                                                                     EMBL:275955; P
se: clone R07B7
                                                                                   235/3; 287/1; 372/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SKF----PILNMLPAFDYSIIECTAELL--HNRTYLGQVDQKI--
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                                                                                                                                                                      PIDN:CAB00115.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 218.5; DB 2; Pred. No. 6.5e-09;
                                                                                                                                                                                                                         from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                           July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                   416/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKCLAEKLEEQQRDWITLPSEKLEM 407
DB 2; 1
7.5e-09;
1es 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188;
                                                                                                                                                                        GSPDB:GN00023; CESP:R0787.6
                                                                                                                                                                                                                                                                                                                               #text_change
                             Length 489;
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Query Match Best Local S Matches 97

ch 9.9%; l similarity 22.0%; 97; Conservative 7

; Score 218; DI ; Pred. No. 7.56 74; Mismatches

Indels

72;

Gaps

18;

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C;Accession: T21566
R;Barlow, K.
submitted to the EMBL Data Library,
A;Reference number: Z19442
A;Accession: T21566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
721566
hypothetical protein F30A10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct 1999 #sequence_revision 15-Oct-1999 #te:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вþ
                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 1
A; Introns: 19/3; 59/3; 93/2; 248/3; 300/1; 348/3; 385/2;
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: C; Genetics:
                 δõ
                                                     B
                                                                            γQ
                                                                                                                           DЪ
                                                                                                                                                           Qy
                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP:F30Al0.4
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:281072; PIDN:CAB03022.1; GSPDB:GN00019; CESP:F30A10.4 A;Experimental source: clone F30A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-486 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIYLVEYSL - - - STSPFVRNRYTH - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVKYIF---NNSIVQDFFAWSKDTYSPDEHFWATLI-RVPGIPGEI-SRSAQDVSDLQSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GFDHGFSYRYNTKAKWTPAGMKLFKIETGVPNEILNRNLIVRKSLNEVIVSKV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETVKPPNSKLERFTYHHELRR--VPYEYVKLPIRTNISKEAPPHNIQIFVGSAYFVLSQA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSLNSGGHGQDPAHFDCLKTILDR--KWDHAIILQNFDLIIKTPYQLSDISESLNYTSIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELKKLNGANML 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAFVRTIYKIYELQEALLSISYHPDNVFCFVMDSKSTDRLKESVRIMSSCFTNVVVLGKE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASKL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIGKSLEIRRRDIID------LEDDDVVAMTSDC-DIYQTLRGYAQKLVSKEEKSFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DINTARVSLQDNGKNSPILRTRSQEKPRKRNITKWMDNYFTADESQF-LNCSEMIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MREMIKRNTAGETPNTQWLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRMTHWDFSGPNGFDKECHSKWKRHGICIMGVEYMNELIKSQQVIANKVMATFDFGTIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRIVKWNYY-EGFFYPSCTGSHLR-SVCIYGAAELRWLIKDGHWFANKFDSKVDPILIKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVKSMFEKLNMDIIIKLFD-DNDYYGVDEMLVQTLYENYLGLEGQMESNCTRNHNDI--L
                                                                                                                                                                                                                                           YTHYKDEVRYEVNCSGIYEQEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGY
                     VSELKKLNGANML-
                                                       ADCFENVIVLDKEYDMDRAGHKQDAAHFDCLKQILDE--HWSHAITLQNFDLIIKSPKQL
                                                                                          AKCESNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFEL
                                                                                                                                 FRDMPPFEKLKRPIAFVRNIYGIYELQEVFLSISYHPDNYFCYAMDSKSSEKLKKSMRIM
                                                                                                                                                                 AQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNL 141
                                                                                                                                                                                                      YYFTESESRY-LNCARLIDGDVESIDTYVNNGR----MKLDEEKLFQLSMDCDSIQ--NRI 142
                                                                                                                                                                                                                                                                         ch 9.7%; Score 213.5; DB 2; l Similarity 23.3%; Pred. No. 1.6e-08; 91; Conservative 71; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #sequence_revision 15-Oct-1999 #text_change
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ETVKPPNSKLERFTYHHELRRVPYE--YVKLPIR
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                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                 49;
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                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                             81
                     246
                                                                                                                                 202
                                                          260
                                                                                              201
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hypothetical protein H41C03.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 2
A;Introns: 48/1; 94/3; 117/3; 220/1; 307/1; 354/3; C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Latreille, P.; Kramer, J.
submitted to the EMBL Data Library, July 1998
A; Description: The sequence of C. elegans cosmid
A; Reference number: 221334
A; Accession: T33384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL;AF077545; PIDN:AAC26306.1; GSPDB:GN00020; A;Experimental source: strain Bristol N2; clone H41C03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-472 <LAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.0
Best Local Similarity 20.9
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420
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                                                                                                                                                                                                                                                                                                                                                                                                      PKKGIY----DPLTTDKQNPMTYEQVVNDLRNEIDQRNAIISELQKDFVKMELKTEFKAIY
                                                                                                                                                                                                                                                                                                                                                                                                                                       WLIKDGHWFANKFDSKVDPILIKCLAEKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FENYLGLDGQMESNC-TVAKEDILTROTHWHLEQSDGLYQDCKSKWLRHSICVIGVEFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I-RVPGIPGEISRSAQDVSDLQSKTRLVKWNYYEG-FFYPSCTGSHLR-SVCIYGAAELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSLNE - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDLSEILNYTSIMGFDYGFTSRYRTFEDWTPAGMKL----FKNE-QSVPLEILHKKLKIR
                                                                                                                                                                                                                                 SKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELKKLNGA
                                                                                                                                                                                                                                                                                                ---IAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIA 151
                                                                                                                                                                                                                                                                                                                                                                    EQEP----LEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVSKEEKSFP-
TDFVS--
                                                                                             LSQAFVKYIFNNSIVQDFF-AWSKDTYSPDEHFWATLIRVP---GIPGEIS-----RS
                                                                                                                                                              NMLETVKPPNSKLERFTYHHELRRVPYEYVKLPI---RTNISKEAPPHNIQIFVGSAYFV
                                                                                                                                                                                                  PDEESVDSAGHNINLAHYNCLRVLINKP-GWNYAILLQNHDVIVKSVYEIEQIYDWLGGA
                                                                                                                                                                                                                                                                   KNGVAFARIVYTDYEMIEKQVQMSYHPQNSFCFAIDKKAPSQFHERLRAMAACLPNVLLL
                                                                                                                                                                                                                                                                                                                                     PRRPETDHIDCGRILADDKVYLQTVSGKDRVKIVENKNLNMSCSAIMNRILPSGNDLKPL 158
                              AQDVSDLQSKTRLVKWNY---YEGFFYP--SCTGSHLRSVCIYGAAE
                                                                  LSRGAVDWMVRTVDLSTYINQWNEGSSGVDEQFIQS-FQVSADLGMPGHFTDECLKQKRN
                                                                                                                                   NDIE-ITPEAGRVDN-----KKFKWDPVSLKMFRNETGIDKNVLTTSMKFAKGAVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T33384
RMSQWMYGSAHKSFDYSIVECTAELLYNRTFLGQVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---VILSKVEVKSLEDKVNLQNVIKREDDRTLEGVDEMMVMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 196.5; DB Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H41C03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394/2; 406/1;
protein H41C03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442/3
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RESULT T24745

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hypothetical protein T09E11.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, October 1996 A; Reference number: Z19930 A; Accession: T24745
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A;Molecule type: DNA
A;Residues: 1-753 <WIL>
Search completed: August 2, 2001, 14:45:51 Job time: 137 sec
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A;Introns: 34/2; 54/2; 191/3; 275/3; 315/3; 359/3; 380/3; 403/3; 426/3; 530/1; 617/1;
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A;Experimental source: clone T09E11
C;Genetics:
A;Gene: CESP:T09E11.6
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Best Local Similarity 21.5
Matches 88; Conservative
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                                                                                                                                                                          337 EGFFYP--SC-TGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPIL 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                         546 NKCLKALLDIP-GWNYALLLQNHDLIMKSVYEMEQIFEWLGGANDIFVT-----
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                                                                                                                           709 ----VPESKCDTNMTRHAVCIIGLEHFQAVASFTHLMFNKVSSSLDELI 753
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21.5%; Pred. No. 6.3e-07;
ative 72; Mismatches 195; Indels
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Title:
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Maximum DB
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length: 2000000000
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Maximum Match 100%
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| SIDS8/gcgdata/geneseq/geneseqp/AA198.DAT:*
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Pred. No. and is derived No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length DB		ID	Description
ь	2194	100.0		22	AAU00037	Human C2GnT3. Ho
N	862	39.3		21	AAB18999	A core 2 beta-1,6
ω	862	39.3		21	AAB18995	A core 2 beta-1,6
4	862	39.3		21	AAY94492	Human C2/4GnT pro
ر. ن	862	39.3		22	AAB30518	Amino acid sequen
6	862	39.3		21	AAB54344	Human pancreatic
7	862	39.3		21	AAB18996	A partial core 2
8	854.5	38.9		19	AAW93942	Rat DH1 protein.
9	849.5	38.7		19	AAW93943	Human core 2 GnT
10	849.5	38.7	428	21	AAB30298	Human heart core
. 11	840.5	38.3		15	AAR51386	Sequence of human

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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Arabidopsis thalia	oseus DAT pro	rabidopsis that	acid se	ne pTB1283-en	dida albic	receptor pro	e KGF re	receptor. M	man secreted F	asmodium f	a	abidopsis thal	abidopsis thali	abidopsis thali	ali	e X	М	bidopsis thal	a	ali	a	Arabidopsis thalia	ali	dopsis thali	e beta-1-6-	beta-1,6-	acid sequ	r catalyti	n beta-1,6-N-	length am	-1,6-N-acet	branching enzym	iabetic

## ALIGNMENTS

AAU00037 standard; Protein; 453

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14-MAY-2001 AAU00037;

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                                                Modified-site
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                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                             /label= "Protein fragment retaining enzyme action force "Used in a fusion protein for in vitro expression studies".
                                           /note=
448
                                                                                                                                   /note=
317
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39..453
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12..32
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                                                                                   "N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              treat such pathological states.
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     241
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                                                                                                         PQKDIYLVEYSLSTSPEVRNRYTHVKDEVRYEVNCSGIYEQEPLEIGKSLEIRRRDIIDL
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)B; AAS00045.
   VKLPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHF
                                                      QWKYVINLCGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEY
                                                                                                                                                                                  edddvvamtsdcdiyqtlrgyaqklvskeeksfpiayslvvhkdaimverlihaiynqhn
                                                                                                                                                                                                       EDDDYVAMTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHN 120
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                                     qwkyvinlcgqdfplksnfelvselkklnganmletvkppnsklerftyhhelrrvpyey
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CLAUSEN H.
                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                              Score 2194; DB 22; Pred. No. 2.9e-190; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                    Length 453;
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                          The present sequence is derived from a human core 2
CC beta-1,6-N-acetylglycosaminyltransferase (core2b GlcNAc-T) polypeptide.
CC The polypeptide can be used to treat diseases and disorders, such as CC cancer, cardiovascular disorders and inflammatory disorders. Such as CC cancer, rheumatoid arthritis, inflammatory bowel disease, arteriosclerosis, septic shock, adult respiratory distress syndrome CC (ARDS) and cancer. Various platelet-mediated pathologies such as CC (ARDS) and cancer. Various platelet-mediated pathologies such as CC athersclerosis and clotting can also be treated. The polypeptides of the invention are predominantly expressed in gastrointestinal tissue CC (stomach, colon, intestine, testis) and are elevated in cancer. CC (astrointestinal disorders that may be prevented or treated include ascites, choicelithiaseis, cirrhosis, Crohn's disease, diverticulitis communo-histochemical analysis, to detect the novel polypeptide and to clocalize it to particular cells and tissues and to specific subcellular collations and to quantitate the level of expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; inflammatory bowel disease; arteriosclerosis; septic shock; adult respiratory distress syndrome; ARDS; cancer; platelet-mediated pathology; athersclerosis; gastrointestinal disorder; clotting; ascites; cholelithiasels; cirrhosis; Crohn's disease; diverticulitis; ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 53; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules of core 2 beta-1,6-N-acetylglycosaminyltransferase useful for providing new compositions for treatment of disorders mediated by the enzyme including cancer, cardiovascular and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-594746/57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Korczak B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lew A;
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99.3%; Similarity 44.5%;

Score 862; DB 21; Pred. No. 9.2e-70;

Length 406;

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RESULT AABIBOLT AABIBOLT AABIBOLT AABIBOT OR AABIT AXX AABIT AXX CORE KW CORE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Core 2 beta-1,6-N-acetylglycosaminyltransferase; core2b GlcNAc-T; cancer; cardiovascular disorder; inflammatory disorder; asthma; rheumatoid arthritis; inflammatory bowel disease; arteriosclerosis; septic shock; adult respiratory distress syndrome; ARDS; cancer; platelet-mediated pathology; athersclerosis; gastrointestinal disorder; clotting; ascites; cholelithiasests; cirrhosis; Crohn's disease; diverticulitis; ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A core 2 beta-1,6-N-acetylglycosaminyltransferase
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                        New nucleic acid molecules of core 2 beta-1,6-N-acetylglycosaminyltransferase useful for providing recompositions for treatment of disorders mediated by the enzyme including cancer, cardiovascular and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                03-FEB-2000; 2000CA-2296936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STSPFVRN-RYTHVKDEVRYEVNCSGIY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGIPGEI-SRSAQDVSDLQSKTRLVKWNYYEGFF-----YPSCTGSHLRSVCIYGAAELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nkkkdpppynltmftgnayivasrdfvghvlknpksgqliewvkdtyspdehlwatlqra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLIKDGHWFANKFDSKVDPILIKCLAEKL 390
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                                                                                                                                                     2000-594746/57.
DB; AAA96569.
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CC beta-1,6-N-acetylglycosaminyltransferase (core2b GlcNAc-T) polypeptide.

CC The polypeptide can be used to treat diseases and disorders, such as CC cancer, cardiovascular disorders and inflammatory disorders including casthma, rheumatoid arthritis, inflammatory bowel disease,

CC arteriosclerosis, septic shock, adult respiratory distress syndrome (ARDS) and cancer. Various platelet-mediated pathologies such as CC the invention are predominantly expressed in gastrointestinal tissue (Stomach, colon, intestina, testis) and are elevated in cancer. CC (astrointestinal disorders that may be prevented or treated include ascites, cholelithiaseis, cirrhosis, Crohn's disease, diverticulitis and ulcerative colitis. The antibodies may be used in colon, intestinal colon colons, the antibodies may be used in colon colons and ulcerative colitis, the antibodies may be used in colons into particular cells and tissues and to specific subceilular colorations and to quantitate the level of expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human core 2
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Sequence 438 DB 21; Length 438;

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Best Local :
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                            362 WLIKDGHWFANKFDSKVDPILIKCLAEKL 390
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                                                                                                                                                                                     NISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRV
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                                                                                                                                                                                                                                                                                                                                                                  RKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVIN 187
                                                                                rwmpgsvpnhpkydisdmtsiarlvkwqghegdidkgapyapcsgihqraicvygagdln
wmlqnhhllankfdpkvddnalqcleeyl 428
                                                                                                                      PGIPGEI-SRSAQDVSDLQSKTRLVKWNYYEGFF-----YPSCTGSHLRSVCIYGAAELR 361
                                                                                                                                                           {\tt nkkkdpppynltmftgnayivasrdfvqhvlknpksqqliewvkdtyspdehlwatlqra}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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44.5%; Pred. No. 1e-69;
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RESULT
AAY94492
AAY94492 standard;
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Protein;
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438

19-SEP-2000 (first entry)

Human C2/4GnT protein

 $\label{eq:human: C2/4GnT: UDP-N-acetylglucosamine: O-glycan biosynthesis: O-glycan beta-1,6-N-acetylglucosaminyltransferase: cancer. \\$ 

Homo sapiens

Location/Qualifiers 10..27 /note= "putative transmembrane

WO200034449-A2

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CX N-acetylgalactcsamine beta-1,6-N-acetylglucosaminyltransferase

CX (C2/4GnT). C2/4GnT is the third member of the family of 0-glycan

CX beta-1,6-N-acetylglucosaminyltransferases. It adds core 2 or core 4

CX based 0-glycans on to oligosaccharides, glycoproteins and

CX depropriately glycosylated glycoconjugates with particular enzymatic,

CX immunogenic, or other biological or physical properties. The nucleotide

CX sequence is useful as a probe for the detection of C2/4GnT from other

CX species and related organisms and for the recombinant production of

CX/4GnT polypeptide. The nucleotide sequence was identified by analysis

CX of EST database sequence information. Oligonucleotides derived from EST

CX clone 17865 of ATCX were used to isolate two full-length C2/4GnT clones

CX performed using Colo205 human cell library by 5' RACE PCR. RT-PCR was

CX performed using Colo205 human cell library by 5' RACE PCR. RT-PCR was

CX performed using Colo205 human cell library by 5' RACE PCR. RT-PCR was

CX cons 17865 of C2/4GnT in Sf9. The control of 0-glycan core assembly

CX has been implicated in tumour progression and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-1999;
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                                                                                                                                                                                                 LCGQDFPLKSNFELVSBLKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRT
                                                                                                                                                                                                                                                   ekspetfkeavkaiiscfpnvfiasklvrvvyaswsrvqadlncmedllqssvpwkyfln
                                                                                                                                                                                                                                                                                                                                                                                                                             STSPEVRN-RYTHVKDEVRYEVNCSGIY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVA 67
WLIKDGHWFANKFDSKVDPILIKCLAEKL
                                  rwmpgsvpnhpkydisdmtsiarlvkwqghegdidkgapyapcsgihqraicvygagdln
                                                                                                         nkkkdpppynltmftgnayivasrdfvqhvlknpksqqliewvkdtyspdehlwatlqra
                                                                                                                                                                                                                                                                      RKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYYIN 187
                                                                                                                                                                                                                                                                                                                      ltrdcehfkaerkfiqfplskeevefpiaysmvihekienferllravyapqniycvhvd
                                                                                                                                                                                                                                                                                                                                                          MTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYD
                                                                                                                                                                                                                                                                                                                                                                                             sqsqycrnilynflklpakrsincsgvtrgdqeavlqailnnlevkkkr-epftdthyls 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                   PGIPGEI-SRSAQDVSDLQSKTRLVKWNYYEGFF-----YPSCTGSHLRSVCIYGAAELR
                                                                                                                                         NISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRV
                                                                                                                                                                        tcgtdfpiksnaemvqalkmlngrnsmesevppkhketrwkyhfevvr---dtlhl----t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schwientek T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 862; DB 2
Pred. No. 1e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 438;
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                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                        beta-1-6-N-acetylglucosaminyltransferase polypeptide, with core2, and I branching activities. It is designated C2GnT-M. C2GnT-M is a membrane protein that is predominantly expressed in colon, small
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New C2GnT-M polypeptides having core 2, core 4 and I branching beta-1-6-N-acetylglucosaminyltransferase activities for preparing reagents useful for diagnosing, preventing or treating inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-040238/05.
N-PSDB; AAC62134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of beta-1-6-N-acetylglucosaminyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB30518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB30518
                                                                                                                                                                                                                                                                 membrane protein that is predominantly expressed in colon, small intestine, trachea, stomach and thyroid, as well as in certain cancer cell lines. C26nT-M polypeptides may be used to prepare molecules having highly branched stalyl Lex and L-selectins, which may be subsequently used to modulate immune reactions, e.g. inflammation and tissue rejection, and to prevent or inhibit tumour metastasis.
                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human beta-1-6-N-acetylglucosaminyltransferas
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 4; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fukuda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-1999;
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                                                                                                                                                                                                                                          Sequence
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                            128
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                                                                                                                                                                                   Local Similarity
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RKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVIN 187
                                                                                  MTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYD 127
                                                                                                             sqsqycrnilynflklpakrsincsgvtrgdqeavlqailnnlevkkkr-epftdthyls 105
                                                                                                                               STSPFVRN-RYTHVKDEVRYEVNCSGIY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVA
                                                      {\tt ltrdcehfkaerkfiqfplskeevefpiaysmvihekienferllravyapqniycvhvd}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
                                                                                                                                                                                                                                             438
                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0233506
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                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 289
                                                                                                                                                                                   39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "potential N-glycosylation site"
                                                                                                                                                                        70;
                                                                                                                                                                     Score 862; DB Pred. No. 1e-6 70; Mismatches
                                                                                                                                                                                        1e-69;
                                                                                                                                                                                                    DB 22;
                                                                                                                                                                        128;
                                                                                                                                                                                                    Length 438;
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AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; cardiant; gene therapy; chromosome mapping;
linkage analysis; tissue identification; tissue typing; forensic
neural; immune system; muscular; reproductive; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1237-1239; 1379pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid that is a pancreatic cancer antigen for preventing, atting, or ameliorating a medical condition, particular pancreatic cer, or for use in assays for diagnosing a pathological condition
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diverticulitis;

ulcerative colitis

Homo

sapiens

03-FEB-1999;

03-FEB-2000; 03-AUG-2000

2000CA-2296936

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                  Core 2 beta-1.6-N-acetylglycosaminyltransferase; core2b GlcNAc-T; cancer; cardiovascular disorder; inflammatory disorder; asthma; rheumatoid arthritis; inflammatory bowel disease; arteriosclerosis; septic shock; adult respiratory distress syndrome; ARDS; cancer; platelet-mediated pathology; athersclerosis; gastrointestinal disorder; clotting; ascites; cholelithiaseis; cirrhosis; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                A partial core 2
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nes 173; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt rwmpgsvpnhpkydisdmtsiarlvkwqghegdidkgapyapcsgihqraicvygagdln}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tcgtdfpiksnaemvqalkmlngrnsmesevppkhketrwkyhfevvr---dtlhl---t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt ekspetfkeavkaliscfpnvfiasklvrvvyaswsrvqadlncmedllqssvpwkyfln}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGIPGEI-SRSAQDVSDLQSKTRLVKWNYYEGFF----YPSCTGSHLRSVCIYGAAELR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wmlqnhhllankfdpkvddnalqcleeyl 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WLIKDGHWFANKFDSKVDPILIKCLAEKL
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                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465
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                                                                                                                                                                                                                                                                                                                                                                                                663
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..1e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a partial human core 2
CC beta-1,6 N-acetyjelycosaminyltransferase (core2b GleNAc-T) polypeptide.
CC The polypeptide can be used to treat diseases and disorders, such as cancer, cardiovascular disorders and inflammatory disorders including casthma, rheumatoid arthritis, inflammatory bowel disease, earteriosclerosis, septic shock, adult respiratory distress syndrome (CC atteriosclerosis, septic shock, adult respiratory distress syndrome (CRDS) and cancer. Various platelet-mediated pathologies such as cathersclerosis and clotting can also be treated. The polypeptides of CC atheristic are predominantly expressed in gastrointestinal tissue (stomach, colon, intestine, testis) and are elevated in cancer. CC Gastrointestinal disorders that may be prevented or treated include ascites, cholelithiasels, cirrhosis, Crohn's disease, diverticulitis cand ulcerative colitis. The antibodies may be used in continuon-histochemical analysis, to detect the novel polypeptide and to coations and to quantitate the level of expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 173; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules of core 2 beta-1,6-N-acetylglycosaminyltransferase useful for providing new compositions for treatment of disorders mediated by the enzyme including cancer, cardiovascular and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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28-JUN-1999
                                  AAW93942;
                                                                     AAW93942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSPEVRN-RYTHYKDEVRYEVNCSGIY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVA 67
                                                                                                                                                                                                                                                                                                                                                                             tcgtdfplksnaemvqalkmlngrnsmesevppkhketrwkyhfevvr---dtlhl---t
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYD 127
                                                                                                                                                                                             WLIKDGHWFANKFDSKYDPILIKCLAEKL
                                                                                                                                                                                                                                  rwmpgsvpnhpkydisdmtslarlvkwqghegdidkgapyapcsgihqraicvygagdln
                                                                                                                                                                                                                                                                       PGIPGEI-SRSAQDVSDLQSKTRLVKWNYYEGFF----YPSCTGSHLRSVCIYGAAELR
                                                                                                                                                                                                                                                                                                         nkkkdpppynltmftgnayivasrdfvqhvlknpksqqliewvkdtyspdehlwatlqra
                                                                                                                                                                                                                                                                                                                                          NISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRV
                                                                                                                                                                                                                                                                                                                                                                                                                LCGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVIN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt ltrdcehfkaerkfiqfplskeevefpiaysmvihekienferllravyapqniycvhvd}
                                                                                                                                                              wmlqnhhllankfdpkvddnalqcleeyl 512
                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  663 AA
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 (first
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                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.3%; score 862; DB 21;
44.5%; Pred. No. 1.9e-69;
tive 70; Mismatches 128;
                                                                         428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 663;
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                                                                                                                                                                                                                                                                                                                                                                                                                       comay be used to prevent or treat cardiomyopathy associated with diabetes and hyperglycaemia. This method involves reacting core 2 GlcNAc-T C (UDP-GlcNAc:Galbetal-3GALNAc-alphaR betta-1,6-N-acetylglucosaminy1-C (TUDP-GlcNAc:Galbetal-3GALNAC-alphaR betta-1,6-N-acetylglucosaminy1-C transferase) with an acceptor substrate and a sugar nuclectide donor in the presence of a test substance under conditions whereby the core 2 GlcNAc-T produces a reaction product, determining the amount of reaction product, and comparing the amount of reaction product with the amount of obtained in the absence of the test substance, where lower amounts of creation product in the presence of the test substance indicate that the cuber transferace in the preventing or treating cardiomyopathy associated with the core 2 GlcNAc-T. The invention also describes (1) methods for preventing or treating cardiomyopathy associated with 2 Gliabetes and hyperglycaemia, and (2) transgenic nonhuman animal whose 2 Germ cells and somatic cells all contain a DNA construct introduced into 2 the animal or an ancestor of the animal at an embryonic stage, where 2 GlicNac-T download a sometic stage and 2 causes the animal to develop cardiomyopathy similar to that associated 2 C with diabetes mellitus and hyperglycaemia. This sequence represents the 2 C rat DH1 protein which is used to describe the method of the invention.
                                                                                                                                                                                                                                                                                            Query Match 38.9
Best Local Similarity 42.1
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for substances that prevent or treat cardiomyopathy associated with diabetes and hyperglycaemia - comprises reacting core 2 GlcNAc-T with acceptor substrate and sugar nucleotide done in presence of test substance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DH1; rat; screening; treatment; prevention; cardiomyopathy; inhibitor; diabetes mellitus; hyperglycaemia; core 2 GlcNac-T; acceptor substrate UDP-GlcNac:Galbetal-3GalNac-alphaR; transgenic animal; germ line;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 3A; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dennis JW, King GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOUN ) MOUNT SINAI HOSPITAL CORP
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                    160
                                                                                                100
                                                                                                                                         74
                                                                                                                                                                             49
                                                                                                                                                                                                                 14
AHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELKKLNGANMLETVKP
                                                                                                                                                                                                              ptkyyfmvlvlslitfsvvrihqkpefvsvshlelsgddpnsnvnctkvlqgdpeeiqkv 73
                                                                                                                                                                                                                                     POKDIYLV-EYSLSTSPFYRNR------YTHYK---DEVRYEVNCSGIYEQEPLEIGK- 48
                                                        VVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASKLEAVEY 159
                                                                                                                                       kleiltvqfkkrprr-----tphdyinmtrdcasfirtrkyimepltkeevgfpiaysi
                                                                                                                                                              SLEI------RRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention describes a method for screening for a substance
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                                                                                                                                                                                                                                                                                                                 38.9%;
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                                                                                                                                                                                                                                                                                              71;
                                                                                                                                                                                                                                                                                                                 Score 854.5; DB 19; Pred. No. 4.8e-69;
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                                                                                                                                                                                                                                                                                                Mismatches
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KW G
                         This invention describes a method for screening for a substance that may be used to prevent or treat cardiomyopathy associated with diabetes and hyperglycaemia. This method involves reacting core 2 GlcNAc-T (UDP-GlcNAc:Galbetal-3GalNAc-alphaR beta-1,6 N-acetylglucosaminyl-transferase) with an acceptor substrate and a sugar nucleotide donor in the presence of a test substance under conditions whereby the core 2 GlcNAc-T produces a reaction product, determining the amount of reaction product, and comparing the amount of reaction product with the amount contained in the absence of the test substance, where lower amounts of creation product in the presence of the test substance indicate that the guidance inhibits core 2 GlcNAc-T. The invention also describes (1) contained for preventing or treating cardiomyopathy associated with the presence of the test substance indicate that the control of the core 2 GlcNAc-T. The invention also describes (1) contained to the presence of the test substance indicate that the control of the contain a DNA construct introduced into the animal or an ancestor of the animal at an embryonic stage, where the animal to develop cardiomyopathy similar to that associated with diabetes meditus and hyperglycaemia. This sequence represents the content of the presents and hyperglycaemia. This sequence represents the content of the presents and hyperglycaemia. This sequence represents the content of the presents and hyperglycaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human core 2 GnT protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening for substances that prevent or treat cardiomyopathy associated with diabetes and hyperglycaemia - comprises reacting core 2 GlORAC-T with acceptor substrate and sugar nucleotide don in presence of test substance
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N-PSDB; AAX24043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig
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Matches 181
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                                                                                                                                                                                                                           07-OCT-1994
                                                                                                                                                                                                                                                                           AAR51386;
                                                                                                                                                                                                                                                                                                                          AAR51386 standard;
                                                                                                 C2GnT; 1-6 AGT;
                          Homo sapiens
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hyperglycemia, comprises administering a subs
2 N-acetylglucosamine-T activity -
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DB; AAC65469.
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                                                                                                                                                                                                                         (first entry)
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                                                                                                    2 beta 1-6 n-acetylglucosaminyltransferase;
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Pred. No. 1.4e
70; Mismatches
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1.4e-68;
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                                                                                                                                                      1-6 AGT)
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycosyltransferases can be isolated by translent expression of in recipient cells, e.g. COS-1. COS-1 cells were transfected with a cDNA library, pcDSR alpha-2F1, constructed from poly(A)+ of activated T lymphocytes which express the C2GnT. Transfected cells were selected using MAD 7305, which identifies a hexasacharide on leukosialin. Leukosialin CD43 is an acceptor molecule for C2GnT activity. A plasmid, pcD5R alpha-Leu, which directed expression of the T305 antigen was identified. The CDNA insert was isolated and sequenced. The cDNA encoded the acceptor molecule leukosialin CD43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New beta 1-6 N-acetyl:glucosaminyl transferase and acceptor used for the study of the effect of variant O-glycan(s) on cell-cell interactions, partic. in cancers
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                                                                                                                                                                                                                       VHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYA 160
                                                                                                                                                                                                                                                                                                          ptkyyfmvlvlslitfsvlr---ihqkpefvsvrhlelagenpssdinctkvlqgdvnei
                                                                                                                                                                                                                                                                                                                                      PQKDIYLV-EYSLSTSPFVRNRYTHVKDE---VRY-----EVNCSGIYEQEPLEI
                                            NNSIVQDFFAWSKDTYSDDEHFWATLIRVPGIPGEISRSAQ-DVSDLQSKTRLVKWNYYE
                                                                                                                                      swsrvqadlncmkdlyamstnwkylinlcgmdfplktnleivrklkllmgennletermp
                                                                                                                                                                   HISRLOADLNCLSDLLKSSIOWKYVINLCGODFPLKSNFELVSELKKLNGANMLETVKPP
                                                                                                                                                                                                                                                     qkvkleiltvkfkkrp--rwtpddyinmtsdcssfikrpkyiveplskeeaefpiaysiv
                                                                                                                                                                                                                                                                                                                                                                   180;
  GFF - - -
                          \verb|qnekiqklmewaqdtyspdeylwatiqripevpgslpashkydlsdmqavarfvkwqyfe|
                                                                                   shkeerw-----kkryevvngkl-tntgtvkmlppletplfsgsayfvvsreyvgyvl
                                                                                                    NSKLERFTYHHELRRVPYEYV--KLPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVKYIF 278
                                                                                                                                                                                               vhhkiemldrllsaiyipqnfycvhvdtksedsylaavmgiascfsnvfvasrlesvvya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an active fragment thereof,
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  -YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEE
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52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= potential N-glycosylation /note= "see also AAs 58 and 95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                42.8%;
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                                                                                                                                                                                                                                                                                                                                                                   Score 840.5; DB 15
Pred. No. 8.8e-68;
0; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catalyses the
                                                                                                                                                                                                                                                                                                                                                                                                 DB 15;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                Preventing or treating cardiomycpathy associated with diabetes mellitus and hyperglycemia, comprises administering a substance that inhibits core 2 N-acetylglucosamine-T activity -
                                                                                                                                                                                                         Sequence
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N-PSDB; AAC65468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diabetic rat heart core 2 GlcNAc~T
                                                                                                                                                                                                                                                                                                                        Example 1; Fig 3B; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishio Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-acetylglucosaminyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat; diabetes; core 2 GlcNAc-T; cardiomyopathy; hyperglycaemia;
UDP-GlcNAc:Galbetal-3GalNAcalphaR betal-6
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                                                                                                                                                                                                                                   in treatment.
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(NISH/) NISHIO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WARR/)
102 HKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 k 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 Q 393
                                                                50
                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gdvskgapyppcdgvhvrsvcifgagdlnwmlrkhhlfankfdvdvdlfaigcldehlrh 420
                                                                                                                 POKDIYLV-EYSLSTSPFVRNR-----YTHVK---DEVRYEVNCSGIYEQEPLEIGKS 49
                                     ----kleiltvgekkrprrtpheytnmtrdcasfirtrkyimepltkeevgfpiaysivv 129
                                                              LEIRRRDIIDLED-----DDVVAMTSDCDIYOTLRGYAQKLVSKEEKSFPIAYSLVV 101
                                                                                       ptkyyfmvlvlslitfevvrihqkpefvsvshlelbgddpnsnvnctkvlqgdpeeiqkv 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) KOYA D.
) DENNIS J W.
) WARREN C E.
                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Koya D,
                                                                                                                                                                                                         427 AA;
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0046876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0943058
                                                                                                                                                                                                                                                                                                                                                                                                                                        King
                                                                                                                                                      38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         GL,
                                                                                                                                        76;
                                                                                                                                                     Score 838;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Warren CE,
                                                                                                                                           Mismatches 130;
                                                                                                                                                     DB 21;
l.5e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Dennis JW
                                                                                                                                                                   Length 427;
                                                                                                                                           Indels
                                                                                                                                          44;
                                                                                                                                       Gaps
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RESULT
AAR71932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                          reverse-transcribed and inserted into expression vector pcDNAI. Plasmid DNA was used to transfect CHO-Py-Leu cells. Transfected cells were screened using human anti-I antigen antibodies and goat anti-human IgM. Plasmid DNA was analyzed to obtain DNA (given in AAQ89201) encoding I-branching enzyme (AAR71932).
                                                                                                                                                         Nucleic acid encoding I-branching enzyme \cdot used to develop prods for treating e.g. inflammatory responses, tumours or hypersensitivity reactions
Sequence
                                                                                                                                                                                                                                                                 Bierhuizen MFA, Fukuda M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-1,6-N-acetylglucosaminyltransferase; I-branching enzyme; IGnT;
inflammation; antiinflammatory; tumor; hypersensitivity; anemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I-branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR71932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR71932 standard; Protein; 400 AA
                                                                                                     Poly-A RNA isolated from human PA-1 teratocarcinoma cells was
                                                                                                                                Disclosure; Fig.6; 56pp; English.
                                                                                                                                                                                                                       N-PSDB; AAQ89201
                                                                                                                                                                                                                                                                                           (LJOL-) LA JOLLA CANCER RES
                                                                                                                                                                                                                                                                                                                          09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                     09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                WO9507020-A
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic animal: I antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 hhkidmldrllraiympqnfycihvdrkaeesflaavqgiascfdnvfvasqlesvvyas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lenkniqkfmewaqdtyspdeflwatiqripevpgslpsshkydlsdmnavarfvkwqif 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIPGEISRSAQ-DVSDLQSKTRLVKWNYY 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nke-----krwkyryvvdgkl-tntgvvkaqpplktplfsgsayfvvtreyvgyv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELKKLNGANMLETVK-PP
                                                                                                                                                                                                                                     1995-123182/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSKLERFTYHHELRRVPYEYV---KLPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVKYI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wsrvkadlncmkdlyrmnanwkylinlcgmdfpiktnleivrklfsftgensletekmpp
 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                          93WO-US08476
                                                                                                                                                                                                                                                                                                                                                       93WO-US08476
                         I-branching enzyme
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Query Match Best Local Similarity Matches 143; Conserv

Conservative

43;

32.4%;

Score 711; DB 16; Pred. No. 4.2e-56; 43; Mismatches 129;

Length 400; Indels

12;

ū

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RESULT 14
AAAP24
AAAP24
ID AAR924
AC AAR924
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-1,6-N-acetylglucosaminyltransferase, I-b
glycosyltransferase; blood group; I antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-1,6-N-acetylglucosaminyltransferase, I-branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR92474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR92474 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-1996
    Human beta-1,6-N-acetyl:glucosaminyl transferase, used to develop prods. for the study, detection pathological conditions involving the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5484590-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130
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pathological
                                                                                                                                                                                                                                                                          Bierhuizen MFA,
                                                                                                                                                                                                                                                                                                                                                 (LJOL-) LA JOLLA CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \verb|alkpppphn|| \verb|tiyfgsayvalsrefanfv|| | hdpravd|| | lqwskdtfspdehfwvt|| | nrip|| | hdpravd|| | lqwskdtfspdehfwvt|| | nrip|| | hdpravd|| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gqdfplktnkeivqylkgfkgknitpgvlppahaigrtkyvhqehlgkelsyv---irtt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WFANKFDSKVDPILIKCLAEKLEEQQR 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIPGEISRSAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYGAAELRWLIKDGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAMSKDTYSPDEHFWATLIRVP 308
                                                                                                                                                          1996-087019/09
DB; AAT16201.
                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0118906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0118906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= N-glycosylation_site 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Membrane-anchoring_do
37
/label= N-glycosylation_site
212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= N-glycosylation_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                 AAW56628 standard; Protein;
                                                                                                                                                                                              IGNT; core 2-beta--1,1-N-acetylglucosaminyltransferase; C2GnT; treatment; disorder; under expression; type-II hypersensitivity reaction; neonatal haemolytic disease; autoimmune haemolytic anaemia;
                                                                                                                                                                                                                                                                         Full length amino acid sequence of human IGnT.
                                                                                                                                                                                                                                                                                                      11-AUG-1998
(LJOL-) LA JOLLA CANCER RES FOUND
                              09-SEP-1993;
                                                          07-JUN-1995;
                                                                                         16-JUN-1998
                                                                                                                                                  Homo sapiens
                                                                                                                                                                               thrombocytopenia.
                                                                                                                                                                                                                                        Human; beta-1,6-N-acetylglucosaminyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequences and their complementary sequences - useful for producing fragment of recombinant human I-branching -1,6-N-acetyl-glucosaminyl-transferase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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361 lfankfelntypltvecl--elrhrer 385
                                      369 WFANKFDSKVDPILIKCLAEKLEEQQR 395
                                                                                                                  309 GIPGEISRSAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYGAAELRWLIKDGH 368
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Local Similarity 43.7%;
les 143; Conservative 4:
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Pred. No. 4.2e-56;
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(without alignments)
793.489 Million cell updates/sec
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FT	Human heart core 2	1 AAB30298	428 2
FΤ	Human core 2 GnT p	9 AAW93943	428 19
FT	Human pancreatic c	1 AAB54344	465 2
FT	Rat DH1 protein.	9 AAW93942	
FT	A partial core 2 b	1 AAB18996	663 21
FT	Amino acid sequenc	2 AAB30518	438 23
ΕŢ	Human C2/4GnT prot		438 2
FT	A core 2 beta-1,6-	1 AAB18995	438 2:
FT	Human C2GnT3. Hom	2 AAU00037	453 23
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RESULT
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                                                                                                                                                                                                                                                                                                   Human; C2GnT3; Thymus-related disorder; cancer; tumour; adenoma; UDP-GlcNAc: Galbeta1,3GalNAc alpha-R beta1,GGlcNAc transferase; sarcoma malignant melanoma; breast cancer; certical cancer; hypoactivity; hyperactivity; atrophy; thymus enlargement; autoimmunity; arthritis; leukaemia; lymphoma; immunosuppression; AIDS; Wiskott-Aldrich syndrome; acquired immunodeficiency syndrome; sepsis; wound healing; infection.
                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                              Human C2GnT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU00037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU00037 standard; Protein; 453 AA.
                                               Modified-site
                                                                                  Modified-site
                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-2001
                   Modified-site
                                                                                                                                                                                   Protein
                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                  /note= "N-glycosylated"
317
                                                                                    /note=
286
/note= "N-glycosylated"
448
/note= "N-glycosylated"
                                                                                                                  /label- "Protein fragment retaining enzyme activity"
/note- "Used in a fusion protein for in vitro
expression studies"
72
                                                                                                                                                                                   /label= "Transmembrane domain" 39..453
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                              "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                 sarcoma;
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Best Local
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UDP-GLONAC: balbecal, bearer again. C2GnT3). C2GnT3 and nucleic acids encoding it are useful in the particularly a thymus-related disorder. C2GnT3, nucleic acids encoding it and antibodies against it may also be used for in vitro purposes related to scientific research, DNA synthesis and manufacture of vectors, in the prognostic and diagnostic evaluation of conditions associated with altered expression or activity of C2GnT3 or conditions by detecting and localising the DNA and protein. Disorders such as tumours (e.g. malignant melanoma, adenoma and sarcoma) and cancers (e.g. of the breast or cervix), hypoactivity, hyperactivity, atrophy, enlargement of the breast or cervix), hypoactivity, hyperactivity, atrophy, enlargement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                breast or červix), hypoactivity, hyperactivity, atrophy, enlargement of thymus, autoimmunity, arthritis, leukaemia, lymphomas, immunosuppression acquired immunodeficiency syndrome (AIDS), Wiskott-Aldrich syndrome, sepsis, wound healing, acute and chronic infection, cell-mediated or humour immunity, or THI/TH2 imbalance, may be treated using these protein or nucleic acid. The antibodies may be used to screen potential therapeutic compounds to determine their effects on a conditions such as thymus-related disorder or cancer, to determine the level of C20nT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents Human UDP-N-acetyl-glucosamine:Galactose-betal, 3-N-acetylgalactosamine-alpha-R betal-6 N-acetylglucosaminyltransferase (UDP-GlcNAc: Galbetal, 3GalNAc alpha-R betal, 6GlcNAc transferase or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New C2GnT3 polypeptides and nucleic acids encoding the polypeptides useful for treating conditions mediated by a C2GnT3 polypeptide, e. thymus-related disorders, cancers, tumours, immunosuppression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schwientek T, Clausen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCHW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Fig 1; 97pp;
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression in cells genetically engineered to produce C2GnT3, or to detect and quantify polypeptides in a sample to determine their role in particular cellular events or pathological states and to diagnose and
                                                                      181
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                                                                                                                                                                                                                                                                    MKIEKCYFKHTLQQKVFILFLTLWLLSLLKLLNVRRLEPQKDIYLVEYSLSTSPFVRNRY
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DB; AAS00045.
                                                                                                                         QKLVSKEEKSFPIAYSLVYHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTEKVAMNNLA 180
                                                                                                                                                                         kcfsnifiaskleaveyahisrlqadlnclsdllkssiqwkyvinlcgqdfplksnfelv
 SELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFV
                                                                                                      qklvskeeksfpiayslvvhkdaimverlihaiynqhniycihydrkapdtfkvamnnla
                                                                    KCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELV
                                                                                                                                                                                                                                                                                                                         453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHWIENTEK T.
CLAUSEN H.
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               pathological states
                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                        Score 2389;
Pred. No. 1
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1.6e-207;
ss '0;
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(stomach, colon, intestine, testis) and are elevated in cancer. Gastrointestinal disorders that may be prevented or treated incl ascittes, cholelithiaseis, cirrhosis, Crohn's disease, diverticul and ulcerative colitis. The antibodies may be used in immuno-histochemical analysis, to detect the novel polypeptide a localize it to particular cells and tissues and to specific subt
                                                                                                                                                                              beta-1,6-N-acetylglycosaminyltransferase (core2b GlcNAc-T) polypeptide. The polypeptide can be used to treat diseases and disorders, such as cancer, cardiovascular disorders and inflammatory disorders including asthma, rheumatoid arthritis, inflammatory bowel disease, arteriosclerosis, septic shock, adult respiratory distress syndrome (ARDS) and cancer. Various platelet-mediated pathologies such as athersolerosis and clotting can also be treated. The polypeptides of the invention are predominantly expressed in gastrointestinal tissue interestinal intestinal tassue invented in cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diverticulitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  septic shock; adult respiratory distress syndrome; ARDS; cancer; platelet-mediated pathology; athersclerosis; gastrointestinal disorder; clotting; ascites; cholelithiaseis; cirrhosis; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Core 2 beta-1,6-N-acetylglycosaminyltransferase; core2b GlcNAc-T;
cancer; cardiovascular disorder; inflammatory disorder; asthma;
rheumatoid arthritis; inflammatory bowel disease; arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-1,6-N-acetylglycosaminyltransferase useful for providing new compositions for treatment of disorders mediated by the enzyme including cancer, cardiovascular and inflammatory disorders. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA2296936-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human core 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecules of core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Korczak B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLYC-) GLYCODESIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 50-51; 66pp;
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         polypeptide and to
specific subcellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human C2/4GnT protein
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                                                                                                                                                                                                                                                                                                                                                            Domain
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                             Clausen
                                                                                                                             04-DEC-1998;
                                                                                                                                                                               03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLAU/) CLAUSEN H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 vtrgdqeavlqailnnlevkkkr-epftdthylsltrdcehfkaerkfiqfplskeevef
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKYIFNNSIVQDFFAMSKDTYSPDEHFWATLIRVPGIPGEI-SRSAQDVSDLQSKTRLVK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lvrvvyaswsrvqadlncmedllqssvpwkyflntcgtdfpiksnaemvqalkmlngrns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LETYKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFVGSAYFVLSQAF 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKL 428
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182; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C2/4GnT;
an beta-1,
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                             Schwientek T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                             98DK-0001605
                                                                                                                                                                               99WO-DK00677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UDP-N-acetylglucosamine; O-glycan biosynthesis;
,6-N-acetylglucosaminyltransferase; cancer.
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 10..27
                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPILIKCLA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.38;
                                                                                                                                                                                                                                                                                                                                 "putative transmembrane domain"
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Pred. No. 4.4e-70;
1; Mismatches 146
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CC (C2/4GnT). C2/4GnT is the third member of the family of O-glycan CC beta-1,6-N-acetylglucosaminyltransferases. It adds core 2 or core 4 CC based O-glycans on to oligosaccharides, glycoproteins and CC glycosphingolipids. C2/4GnT can therefore be used in the production of CC glycosphingolipids. C2/4GnT can therefore be used in the production of CC immunogenic, or other biological or physical properties. The nucleotide CC immunogenic, or other biological or physical properties. The nucleotide Sequence is useful as a probe for the detection of C2/4GnT from other CC c2/4GnT polypeptide. The nucleotide sequence was identified by analysis CC c2/4GnT polypeptide. The nucleotide sequence was identified by analysis CC cone 17865 of ATCC were used to isolate two full-length C2/4GnT clones CC from a human foreskin genomic plilibrary by 5' RACE pCR. RT-PCR was CC for expression of C2/4GnT in sf9. The control of O-glycan core assembly has been implicated in tumour progression and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is human UDP-N-acetylglucosamine:
N-acetylgalactosamine beta-1.6-N-acetylglucosaminyltransferase
(C2/4GnT): C2/4GnT is the third member of the family of O-glycc
beta-1.6-N-acetylglucosaminyltransferases. It adds core 2 or oc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule encoding UDP-N-acetylglucosamine useful as probe for the detection of specified glucoseaminyltransferase from other species and related organisms
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N-PSDB; AAA48623.
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Sequence

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                                                                                                                                                                                    vtrgdqeavlqailnnlevkkkr-epftdthylsltrdcehfkaerkfiqfplskeevef
                                                                                                                                                                                                                                                                                                                                                 lwalgcymllatvalklsfrikcdsdhlglesresgsgycrnilynflklpakrsincsg 72
                                                                                                                                    mesevppkhketrwkyhfevvr---dtlhl---tnkkkdpppynltmftgnaylvasrdf
                                                                                                                                                                                                                                          piaysmvihekienferllravyapqniycvhvdekspetfkeavkaliscfpnvfiask
                                                                                                                                                                                                                                                                 PIAYSLYVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASK 191
                                                                                                                                                                                                                                                                                                                       IY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVSKEEKSF 131
                                                                                                                                                                                                                                                                                                                                                                                                       182;
    EKL 428
                         \verb|wqghegdidkgapyapcsgihqraicvygagdlnwmlqnhhllankfdpkvddnalqcle|\\
                                                    WNYYEGFF----YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPILIKCLA 425
                                                                               vqhvlknpksqqliewvkdtyspdehlwatlqrarwmpgsvpnhpkydisdmtsiarlvk
                                                                                                VKYIFNNSIVQDFFAWSKDIYSPDEHFWATLIRVPGIPGEI-SRSAQDVSDLQSKTRLVK
                                                                                                                                                            LETYKPPNSKLERFTYHHELRRYPYEYYKLPIRTNISKEAPPHNIQIFYGSAYFYLSQAF
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                                                                                                                                                                                                                                                                                                                                                                                                                     36.38;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 868; DB 21;
Pred. No. 4.4e-70;
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 438;
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RESULT
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ID AAB3
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AC AAB3
XX

AAB30518;

AAB30518 standard;

Protein;

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Best Local
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human beta-1-6-N-acetylglucosaminyltransferase polypeptide, with core2, core4 and I branching activities. It is designated C2GnT-M. C2GnT-M is a membrane protein that is predominantly expressed in colon, small intestine, trachea, stomach and thyroid, as well as in certain cancer cell lines. C2GnT-M polypeptides may be used to prepare molecules having highly branched sialyl Lex and L-selectins, which may be subsequently used to modulate immune reactions, e.g. inflammation and tissue rejection, and to prevent or inhibit tumour metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New C2GnT-M polypeptides having core 2, core 4 and I branching beta-1-6-N-acetylglucosaminyltransferase activities for prepar reagents useful for diagnosing, preventing or treating inflamm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukuda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JAN-1999;
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DB; AAC62134.
                                                                   LEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELKKLNGANM
                                                                                                                                                               vtrgdqeavlqailnnlevkkkr-epftdthylsltrdcehfkaerkfiqfplskeevef
mesevppkhketrwkyhfevvr---dtlhl---tnkkkdpppynltmftgnayivasrdf
                                                                                                          piaysmvihekienferllravyapqniycvhvdekspetfkeavkaiiscfpnvfiask
                                                                                                                                    PIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASK
                                                                                                                                                                                           IY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVSKEEKSF
                                                                                                                                                                                                                    {\tt lwalgcymllatvalklsfrlkcdsdhlglesresqsgycrnilynflklpakrsincsg}
                                                                                                                                                                                                                                                                            182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid
                          LETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFVGSAYFVLSQAF
                                                      lvrvvyaswsrvqadlncmedllqssvpwkyflntcgtdfpiksnaemvqalkmlngrns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-1-6-N-acetylglucosaminyltransferase; C2GnT-M; ne protein; branched sialyl Lex; L-selectin; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BURNHAM
                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                              438
                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of beta-1-6-N-acetylglucosaminyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rejection; tumour
                                                                                                                                                                                                                                                                                       36.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "potential N-glycosylation
                                                                                                                                                                                                                                                                          Score 868; DB 22;
Pred. No. 4.4e-70;
1; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-selectin;
metastasis.
                                                                                                                                                                                                                                                                                                     Length 438;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune reaction;
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inflammation
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                                                                                                                                                                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                              The present sequence represents a partial human core 2
The polypeptide can be used to treat diseases and disorders, such as cancer, cardiovascular disorders and inflammatory disorders including asthma, rheumatoid arthritis, inflammatory bowel disease, arteriosclerosis, septic shock, adult respiratory distress syndrome (ARDS) and cancer. Various platelet-mediated pathologies such as athersclerosis and clotting can also be treated. The polypeptides of the invention are predominantly expressed in gastrointestinal tissue (stomach, colon, intestine, testis) and are elevated in cancer. Gastrointestinal disorders that may be prevented or treated include ascites, cholelithiasels, cirrhosis, Crohn's disease, diverticulitis and ulcerative colltis. The antibodies may be used in immuno-histochemical analysis. to date of the contraction of the incomplete collitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rhounatoid arthritis; inflammatory bowel disease; arteriosclerosis; septic shock; adult respiratory distress syndrome; ARDS; cancer; platelet-mediated pathology; athersclerosis; gastrointestinal disor clotting; ascites; cholelithiaseis; cirrhosis; Crohn's disease; diverticulitis; ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Core 2 beta-1,6-N-acetylglycosaminyltransferase; core2b GlcNAc-T;
cancer; cardiovascular disorder; inflammatory disorder; asthma;
                                                                                                                                                                                                                                                                                                                         New nucleic acid molecules of core 2 beta-1,6-N-acetylglycosaminyltransferase useful for providing recompositions for treatment of disorders mediated by the enzyme including cancer, cardiovascular and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB18996 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-2000;
                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Korczak B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312
                                              immuno-histochemical analysis, t
localize it to particular cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vghvlknpksqqliewvkdtyspdehlwatlqrarwmpgsvpnhpkydisdmtsiarlvk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        2000-594746/57
                                                                                                                                                                                                                                                                                              3; Page 52; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428
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                               and to quantitate the
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lew A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000CA-2296936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 beta-1,6-N-acetylglycosaminyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                  level of expression
                                              tissues and to specific sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drome; ARDS; cancer;
gastrointestinal disorder;
                                                   subcellular
                                                                                                                                                                                                                                                                                                                                                             new
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Query Match Best Local Matches

182;

Conservative

71;

Mismatches

146;

24;

Gaps

9

Similarity

36.3%; 43.0%;

Score 868; DB 21; Pred. No. 8.1e-70;

Length Indels

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RESULT
AAW93942
ID AAW9
XX AAW9
XX AAW9
XX BAH1;
XX DH1;
XX DH1;
XX UDP
XX CA21
XX Ratt
XX Beta
XX Fatt
XX Dec CA21
XX Dec CA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D,
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Screening for substances that prevent or treat cardiomyopathy associated with diabetes and hyperglycaemia - comprises react core 2 GlcNAc-T with acceptor substrate and sugar nucleotide of the core in the core of the core o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DH1; rat; screening; treatment; prevention; cardiomyopathy; inhibitor; diabetes mellitus; hyperglycaemia; core 2 GLNAC-T; acceptor substrate; UDP-GlCNAc:Galbetal-3GalNAc-alphaR; transgenic animal; germ line; beta-1,6-N-acctylglucosaminyl-transferase.
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transferase) with an acceptor substrate and a sugar nucleotide donor in CC the presence of a test substance under conditions whereby the core 2 CC GleNAc-T produces a reaction product, determining the amount of reaction product, and comparing the amount of reaction product with the amount CC product, and comparing the amount of reaction product with the amount of reaction product in the presence of the test substance indicate that the CC reaction product in the presence of the test substance indicate that the CC methods for preventing or treating cardiomyopathy associated with CC diabetes and hyperglycaemia, and (2) transgenic nonhuman animal whose CC germ cells and somatic cells all contain a DNA construct introduced into the animal or an ancestor of the animal at an embryonic stage, where CC incorporation of the DNA construct into the germ line of the animal CC causes the animal to develop cardiomyopathy similar to that associated with diabetes mellitus and hyperglycaemia. This sequence represents the CC rat DH1 protein which is used to describe the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            may be used to prevent or treat cardiomyopathy associated with diabetes and hyperglycaemia. This method involves reacting core 2 GlcNAc-T (UDP-GlcNAc:Galbetal-3GalNAc-alphak beta-1,6-N-acetylglucosaminyl-
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig
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428 AA;
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36.38;

19;

Length

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Best Local S
Matches 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                        28 LLKLLNYRRLF--PQKDIYLV-EYSLSTSPFVRNR----YTHVK---DEVRYEVNCS 74
                                                                                                                                                                                                                                                                                                                                                                                                            1 mlrnlfrrrlfsyptkyyfmvlvlslitfsvvrihgkpefvsvshlelsgddpnsnvnct
                                                                                                                                                                                                                                 avarfvkwqyfegdvsngapyppcsgvhvrsvcvfgvgdlswmlrkhhffankfdmdvdp
                                                                                                               fvvtreyvgyvlenkniqkfmewaqdtyspdeflwatiqripevpgslpsshkydlsdmn
                                                                                                                                                                       sftgensletekmppnkeerwk-----krytvvdgkl-tntgvvkaqpplktplfsgsay
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                                                                                                                                                                                                                                                 NIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELK 244
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falqcleehlrhk 421
                            ILIKCLAEKLEEQ
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                                                                                                                                                                                                                                                                                                                      SKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFS
                                                                                    SKTRLVKWNYYEGFF----YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDP
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                            431
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Pred. No. 5.8e-70;
3; Mismatches 136
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AAB54344
ID AAB5
XX
AC AAB6
XX
DT 09-N
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DE Huma

AAB54344; 09-MAR-2001

AAB54344 standard;

Protein; 465

7

Human pancreatic cancer antigen

protein sequence

SEQ

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NO:796

(first entry)

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                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11;
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                                                                                                                                                                                                                          23 LWLLS---LLKLLNVRRLFPQK---DIYLVEYSLSTSPFVRN-RYTHVKDEVRYEVNCSG
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DB; AAC99109.
piaysmvihekienferllravyapqniycvhvdekspetfkeavkaiiscfpnvfiask
                                           PIAYSLVVEKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASK 191
                                                                                        vtrgdqeavlqailnnlevkkkr-epftdthylsltrdcehfkaerkfiqfplskeevef
                                                                                                                                                                               lwalgcymllatvalklsfxlkcdsdhlglesresqsqycrnilynflklpakrsincsg
                                                                                                                                    IY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVSKEEKSF
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                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      465
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43.0%;
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Pred. No. 7.3e-70;
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Screening; treatment; prevention; cardiomyopathy; inhibitor; diabetes mellitus; hyperglycaemia; core 2 GlcNac-T; acceptor UDP-GlcNac:Galbetal-3GalNac-alphak; transgenic animal; germ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW93943 standard; Protein;
                                                                                                                                                Screening for substances that prevent or treat cardiomyopathy associated with diabetes and hyperglycaemia - comprises reacting core 2 GlaNAC-T with acceptor substrate and sugar nucleotide donor in presence of test substance
                                                                                                                                                                                                                                                                                                                                     CA2186987-A.
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                                                                                                                               Disclosure; Fig 9; 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                             GnT protein
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                                                                                                                                                                                                                                   Nishio Y,
                                                                                                                                                                                                                                   Warren CE;
                                                                                                                                                                                                                                                                                                                                                                              Ac-T; acceptor substrate;
animal; germ line;
an; core 2 GnT.
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transferase) with an acceptor substrate and a sugar nucleotide donor in the presence of a test substance under conditions whereby the core 2 GlcNAc-T produces a reaction product, determining the amount of reaction product with the amount obtained in the absence of the test substance, where lower amounts of reaction product in the presence of the test substance indicate that the substance inhibits core 2 GlcNAc-T. The invention also describes (1) methods for preventing or treating cardiomyopathy associated with

may be used to prevent or treat cardiomyopathy associated with diabetes and hyperglycaemia. This method involves reacting core 2 GlcNAc-T (UDP-GlcNAc:Galbetal-3GalNAc-alphaR beta-1,6-N-acetylglucosaminyl-

invention

describes a method

for screening

for a substance

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                                                                                                                                                                                                                                                                                       AAB30298 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                              Human; diabetes; core 2 GlcNAc-T;
UDP-GlcNAc:Galbetal-3GalNAcalphaR
                                                                                                                                                                                                       Human heart
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              02-OCT-1996;
                                        02-OCT-1997;
                                                                 17-OCT-2000
                                                                                             US6131578-A
                                                                                                                        Homo
                                                                                                                                                N-acetylglucosaminyltransferase
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                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187;
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              96US-0046876
                                        97US-0943058
                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                          421
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43.1%;
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                                                                                                                                                                                                                                                                                       428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                              cardiomyopathy; hyperglycaemia;
betal-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132;
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RESULT AAB18999 ID AAB

standard;

Peptide; 406

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A core 2 beta-1,6-N-acetylglycosaminyltransferase catalytic

AAB18999 st; AAB18999; 08-FEB-2001

(first

entry)

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Best Local S
Matches 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes the human UDP-GlCNAc:Galbetal-3GalNAc alphaR betal-6 N-acetylglucosaminyltransferase (core 2 GlCNAc-7) protein and coding sequences. The enzyme is associated with cardiomyopathy in diabetes and hyperglycaemia sufferers. The invention also provides methods for identifying inhibitors of core 2 GlCNAc-T which can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preventing or treating cardiomyopathy associated with diabetes meilitus and hyperglycemia, comprises administering a substance that inhibits core 2\ N-acetylglucosamine-T activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DENN/)
(WARR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 9; 21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KING/)
(NISH/)
(KOYA/)
                        418
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408
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                                                                                                                                                                                                                                                                                                                                                                                     28 LLKLLNVRRLF--PQKDIYLV-EYSLSTSPFVRNRYTHVKDE---VRY-----EV 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment.
                                                                                                 2000-678642/66
DB; AAC65469.
lfaiqcldehlrhk 421
                        PILIKCLAEKLEEQ
                                              qavarfvkwqyfegdvskgapyppcdgvhvrsvcifgagdlnwmlrkhhlfankfdvdvd
                                                             QSKTRLVKWNYYEGFF-----YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVD
                                                                                                                                                                            LNGANMLETYKPPNSKLERFTYHHELRRVPYEYV--KLPIRTNISKEAPPHNIQIFVGSA
                                                                                                                                                                                                                                                                      KEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTEKVAMNNLAKCFSN 185
                                                                                                                                                                                                                                                                                                                                 NCSGIYEQEPLEIGK-----SLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVS 125
                                                                                                                                                    lmgennletermpshkeerw-----kkryevvngkl-tntgtvkmlppletplfsgsa
                                                                                                                                                                                                     vfvasrlesvvyaswsrvqadlncmkdlyamsanwkylinlcgmdfpiktnleivrklkl
                                                                                                                                                                                                                              IFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELKK 245
                                                                                                                                                                                                                                                       keeaefpiaysivvhhkiemldrllraiympqnfycvhvdtksedsylaavmgiascfsn
                                                                                                                                                                                                                                                                                                         nctkvlqgdvneiqkvkleiltvkfkkrp--rwtpddyinmtsdcssfikrrkyivepls
                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
187; Conserv
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NISHIO Y.
KOYA D.
DENNIS J WARREN C F
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                          431
                                                                                                                                                                                                                                                                                                                                                                                                                        36.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                            72;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 863.5; DB 21; Pred. No. 1.1e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Warren
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               132;
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CC The polypeptide can be used to treat diseases and disorders, such as
CC cancer, cardiovascular disorders and inflammatory disorders including
CC asthma, rheumatoid arthritis, inflammatory bowel disease,
CC carter; cardiovascular disorders and inflammatory distress syndrome
CC arteriosclerosis, septic shock, adult respiratory distress syndrome
CC (ARDS) and cancer. Various platelet-mediated pathologies such as
CC (ARDS) and cancer. Various platelet-mediated pathologies such as
CC (Stomach, colon, intesting can also be treated. The polypeptides of
CC (Stomach, colon, intestine, testis) and are elevated in cancer.
CC (Sastrointestinal disorders that may be prevented or treated include
CC ascites, cholelithiaseis, cirrhosis, crohn's disease, diverticulitis
CC and ulcerative colitis. The antibodies may be used in
CC conception and to particular cells and tissues and to specific subcellular
CC localize it to particular cells and tissues and to specific subcellular
CC locations and to quantitate the level of expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Core 2 beta-1,6-N-acetylglycosaminyltransferase; core2b GlcNAc-T; cancer; cardiovascular disorder; inflammatory disorder; astima; rheumatorid arthritis; inflammatory bowel disease; arteriosclerosis; septic shock; adult respiratory distress syndrome; ARDS; cancer; platelet-mediated pathology; athersclerosis; gastrointestinal disorder; clotting; ascites; cholelithiaseis; cirrhosis; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-1,6-N-acetylglycosaminyltransferase useful for providing new compositions for treatment of disorders mediated by the enzyme including cancer, cardiovascular and inflammatory disorders. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diverticulitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-594746/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules of core 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLYC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                       194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
173;
   286
                                                                                                                                                                                                                                                               166
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sqsqycrnilynflklpakrsincsgvtrgdqeavlqailnnlevkkkr-epftdthyls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STSPFVRN-RYTHVKDEVRYEVNCSGIY--EQEPL--EIGKSLEIRRRDIIDLEDDDVVA 105
                                                                                                                              LCGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRT
                                                                                                                                                                                              RKAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVIN
                                                                                                                                                                                                                                                                                                                                                              MTSDCDIYQTLRGYAQKLYSKBEKSFPIAYSLYVHKDAIMVERLIHAIYNQHNIYCIHYD
      NISKEAPPHNIQIFYGSAYFYLSQAFYKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRV
                                                                                                                                                                                                                                                                                                                            ltrdcehfkaerkfiqfplskeevefpiaysmvihekienferllravyapqniycvhvd
                                                                tcgtdfpiksnaemvqalkmlngrnsmesevppkhketrwkyhfevvr--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Page 53; 66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCODESIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0118674
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44.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 862; DB 21;
Pred. No. 1.4e-69;
70; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 406;
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δÃ В QyВ QΥ 밁 VΩ

Sequence

428

35.8%;

Score

854. . 5 В 15;

Length

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                         C2GnT, or an active fragment thereof, catalyses the formation of critical branches in O-glycans. cDNAs encoding various glycosyltransferases can be isolated by transient expression of cDNA in recipient cells, e.g. COS-1. COS-1 cells were transfected with a cDNA library, pcDSR alpha-2F1, constructed from poly(A)+ RNA of activated T lymphocytes which express the C2GnT. Transfected cells were selected using MAb T305, which identifies a hexasaccharide on leukosialin. Leukosialin CD43 is an acceptor molecule for C2GnT activity. A plasmid, pcDSR alpha-Leu, which directed expression of the T305 antigen was identified. The CDNA insert was isolated and sequenced. The cDNA encoded the acceptor molecule leukosialin CD43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of human core 2 beta 1-6 N-acetylglucosaminyltransferase (
                                                                                                                                                                                                                                                New beta 1-6 N-acetyl:glucosaminyl transferase and acceptor used for the study of the effect of variant O-glycan(s) on cell-cell interactions, partic. in cancers
                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP590747-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o-glycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR51386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR51386 standard;
                                                                                                                                                                                                                                                                                                                                                          Bierhuizen MFA,
                                                                                                                                                                                                                                                                                                                                                                                     (LJOL-) LA JOLLA CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2GnT; 1-6 AGT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
                                                                                                                                                                                                                       Disclosure; Page 20-22; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGIPGEI-SRSAQDVSDLQSKTRLVKWNYYEGFF----YPSCTGSHLRSVCIYGAAELR
                                                                                                                                                                                                                                                                                                              AAQ61559
                                                                                                                                                                                                                                                                                                                                                                                                                    9205-0955041
                                                                                                                                                                                                                                                                                                                                                                                                                                               93EP-0250268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      core 2 beta 1-6 n-acetylglucosaminyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 10..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= potential N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= signal/membrane anchoring domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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Local

42.9%;

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Indels

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Gaps

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XX AAB33
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XX PAL:

DT 12-F
XX Rat;

XX UDP-
XX US61

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; diabetes; core 2 GlcNAc-T; cardiomyopathy; hyperglycaemia; UDP-GlcNAc:Galbetal-3GalNAcalphaR betal-6 N-acetylglucosaminyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diabetic rat heart core 2 GlcNAc-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB30297 standard;
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Preventing or treating cardiomyopathy associated with diabetes mellitus and hyperglycemia, comprises administering a substance that inhibits
                                                                                                                                                                                                                                                                                                                                                                        02-OCT-1996;
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                                                                                                                                                                                                                                                                (KING/) KING G L.
(NISH/) NISHIO Y.
(KOYA/) KOYA D.
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DB; AAC65468.
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86; Conservative
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WARREN C
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2; Mismatches 133;
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RESULT 13
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Query Match 35.6
Best Local Similarity 40.9
Matches 178; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3B; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         core 2 N-acetylglucosamine-T activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                               inflammation; antiinflammatory; transgenic animal: I antigen.
                                                                                                                                                                  I-branching enzyme
                                                                                                                                                                                            23-SEP-1995
                                                                                                                                                                                                                                              AAR71932 standard; Protein;
                                                                                       Homo sapiens
                                                                                                                            Beta-1,6-N-acetylglucosaminyltransferase: I-branching enzyme;
inflammation; antiinflammatory; tumor; hypersensitivity; anem
                                                                                                                                                                                                                       AAR71932;
                                     16-MAR-1995
                                                              WO9507020-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIPGEISRSAQ-DVSD
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40.9%; Pred. No. 1.8e-68;
tive 78; Mismatches 133
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09-SEP-1993;

93WO-US08476

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding I-branching enzyme - used to develop prods. for treating e.g. inflammatory responses, tumours or hypersensitivity reactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bierhuizen
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                                                                                                                                                                                     glycosyltransferase;
                                                                                                                                                                                                                                                                 Beta-1,6-N-acetylglucosaminyltransferase, I-branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                          AAR92474 standard; Protein; 400
  Modified-site
                                                                               Key
                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                       22-APR-1996
                                                        Domain
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hes 143;
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DB; AAQ89201.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \verb|attefkdaveqllscfpnaflaskmepvvyggisrlqadlncirdlsafevswkyvintc|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gqdfplktnkeivqylkgfkgknitpgvlppahaigrtkyvhqehlgkelsyv---irtt
                                                                                                                                                                                     ,6-N-acetylglucosaminyltransferase,
yltransferase; blood group; I antig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                       (first entry)
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     /label= Membrane-anchoring_domain 37
                                                     Location/Qualifiers 7...25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%;
43.7%;
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Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ore 711; DB 16;
red. No. 5.9e-56;
Mismatches 129;
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                                                                                                                                                                                          I antigen;
                                                                                                                                                                                                                 I-branching
                                                                                                                                                                                        polylactosaminoglycan
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                                                                                                                                                                                                                    IGnT;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                   Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human beta-1,6-N-acetyl:glucosaminyl transferase, - used to develop prods. for the study, detection pathological conditions involving the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IGnT) (AAR92474) is an enzyme that converts blood group i antigen to Initigen. The occurrence of I antigen is associated with development and maturation of erythroid cells. Membrane-bound or soluble forms of IGnT are obtd. by expression of encoding DNA sequences (see AAT16201) in host cells. IGnT is used to study the role of IGnT in development and oncogenesis, to alleviate disorders associated with IGnT underexpression (e.g. haemolytic disease of the newborm, haemolytic anemia and thrombocytopenia), to regulate IGnT expression, and in detection and diagnostic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Column 31-34; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-087019/09
N-PSDB; AAT16201.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human beta-1,6-N-acetylglucosaminyltransferase,
 361
                            407
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                                                                                                                                                                                                                                                               168
                                                                                                                                                                                                                                                                                           70
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                    SDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRK 167
                                                                                                                                                                                                                                                                                        ssckeyltqshyitaplskeeadfplayimvihhhfdtfarlfraiympqniycvhvdek 129
lfankfelntypltvecl--elrhrer
                             WFANKFDSKVDPILIKCLAEKLEEQQR 433
                                                                                    GIPGEISRSAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYGAAELRWLIKDGH 406
                                                                                                                 alkpppphnltiyfgsayvalsrefanfvlhdpravdllqwskdtfspdehfwvtlnrip
                                                                                                                                                                     gqdfplktnkeivqylkgfkgknitpgvlppahaigrtkyvhqehlgkelsyv---irtt 246
                                                                                                                                                                                                  GODFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTY-HHELRRVPYEYVKLPIRTN 286
                                                                                                                                                                                                                                 attefkdaveqllscfpnaflaskmepvvyggisrlqadlncirdlsafevswkyvintc
                                                                                                                                                                                                                                               APDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLC 227
                                                        gvpgsmpnas--
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255
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                                                         -wtgnlraikwsdmed-rhggchghyvhgiciygngdlkwlvnsps
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43.7%;
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                                                                                                                                                                                                                                                                                                                                                   Score 711; DB 17;
Pred. No. 5.9e-56;
3; Mismatches 129;
   385
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ood group i antigen
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and treatment
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW56628 standard; Protein; 400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human beta-1.6-N-acetylglucosaminyltransferase, the I-branching enzyme (IGnT). The protein sequence has a type II transmembrane topology that consists of a short amino terminal cytoplasmic sequence, a signal-anchor sequence followed by a short stem region and a large carboxyl terminal catalytic domain. The protein shows some homology to core 2-beta-1.1-N-acetylglucosaminyltransferase (2GnT). The nucleic acid sequence is used for producing IGnT polypeptides, which can be used to treat disorders arising from under expression of IGnT, e.g. increased to treat disorders arising from under expression such as neonatal susceptibility to type-II hypersensitivity reactions such as neonatal susceptibility to type-II hypersensitivity reactions such as neonatal susceptibility to type-II mypersensitivity reactions and thromborytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences and their complementary sequences - useful for producing fragment of recombinant human I-branching -1,6-N-acetyl-glucosaminyl-transferase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bierhuizen MFA,
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                                                                                                                                                                                                                                                                                                                                                                                               108 SDCDIYQTLRGYAQKLYSKEEKSFPIAYSLYVHKDAIMYERLIHAIYNQHNIYCIHYDRK 167
                                                                                                                                                                                                                                                                                             168
287 ISKEAPPHNIOIFYGSAYFYLSOAFYKYIFNNSIVODFFAWSKDTYSPDEHFWATLIRVP
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                                                                                                                                                                  228
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nes 143; Conserv
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                                                                                           gqdfplktnkeivqylkgfkgknitpgvlppahaigrtkyvhqehlgkelsyv---irtt
                                                                                                                                                               GODFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTY-HHELRRVPYEYVKLPIRTN 286
                                                                                                                                                                                                                         {\tt attefkdaveqllscfpnaflaskmepvvyggisrlqadlncirdlsafevswkyvintc}
                                                                                                                                                                                                                                                                                  APDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLC 227
                                                                                                                                                                                                                                                                                                                                                          400 AA;
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Pred. No. 5.9e-56;
13; Mismatches 129;
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407 WFANKFDSKVDPILIKCLAEKLEEQQR 433
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                               gvpgsmpnas----wtgnlraikwsdmed-rhggchghyvhgiciygngdlkwlvnsps 360
                                                               GIPGEISRSAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYGAAELRWLIKDGH 406
                                                                                              \verb|alkpppphnltiyfgsayvalsrefanfvlhdpravdllqwskdtfspdehfwvtlnrip|
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Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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beta-1,6-N-acetylg
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4.3	4.3	4.3	4.3	<u>4</u> دی	4.3	4.3	4.3	4.4	4.4	4.4	5	4.5	4.5	4.5	4.5
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363 QSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVD 417  :	304 YEVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIPGEISRSAQ-DVSDL 362    : ::  :  :  :  ::  ::  ::  ::  :: ::	246 LNGANMLETVKPDNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFYGSA 303               :   :   :   :	186 IFJASKLEAVEYAHISRLOADLNCLSDLLKSSIQWKYVINLGGODFPLKSNFELVSELKK 245 	126 KEEKSEPIAYSLVYHKDAIMVERLIHAIYNQHNIYGIHYDRKAPDTEKVAMNNLAKGESN 185 	72 NCSGIYEQEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVS 125 	28 LLKLLNVRRLFPQKDIYLV-EYSLSTSPFVRNRYTHVKDBVRYEV 71	Query Match 36.1%; Score 863.5; DB 2; Length 428; Best Local Similarity 43.1%; Pred. No. 6.2e-56; Matches 187; Conservative 72; Mismatches 132; Indels 43; Gaps 12;	ule ty dues: 1 dues: 1 dues: 1 dues: 1 dues: 1 dues: 1 dues: 1	C.Accession: A46293 R;Bierhuizen, M.F.; Fukuda, M. Proc. Natl. Acad. Sci. U.S.A. 89, 9326-9330, 1992 A;Title: Expression cloning of a cDNA encoding UDP-GlcNAc:Gal beta 1-3-GalNAc-R (GlcN A;Reference number: A46293; MUID:93028457 A.Accession: A46293	RESULT 1 A46393 beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase C.Species: Homo sapiens (man) C.Pate: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

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RESULT
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beta-1,
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A;Title: Expression of the developmental A;Reference number: A46297; MUID:93194065
A;Accession: A46297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: nucleic acid

A; Residues: 1-400 <8152

A; Cross-references: GB:Z19550; NID:9296531; PIDN:CAA79610.1; PID:9296532

A; Note: sequence extracted from NCBI backbone (NCBIN:127166, NCBIP:127167)

C; Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
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A; Gene: CESP:F22D6.11
A; Map position: 1
A; Introns: 65/3; 95/2; 136/3; 180/3; 256/3; 281/3; 403/3
                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosldues: 1-445 <WIL>
A;Cross:references: EMBL:Z71262; PIDN:CAA95817.1; GSPDB:GN00019; CESP:F22D6.11
A;Experimental source: clone F22D6
                                                                                                                                                                                  R:Wilkinson, J.
submitted to the EMBL Data Library,
A:Reference number: Z19397
A:Accession: T21262
                                                                                                                                                                                                                                                                                     hypothetical protein F22D6.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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43; Conservative
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hypothetical protein C54C8.11 - Caenorhabditis elegans C,Species: Caenorhabditts elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C,Accession: T20207; T27478 R,Dobson, R.
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δ
                                                                                             A; Map position: A; Introns: 29/2;
                                                                                                                                                                 A;Cross-references: EMBL:AL032664; PIDN:CAA21769.1; A;Experimental source: clone Y91F4A
                                                                                                                                                                                                                                                           A; Reference number: A; Accession: T27478
                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, October 1998 A; Reference number: Z20372
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: T20207
                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data A; Reference number: 219237
                                                                                                                                A; Gene: CESP:C54C8.11
                                                                                                                                                                                                        A; Residues:
                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                 R;McLay,
                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone C54C8
                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                        A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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   Best Local Similarity Matches 102; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 TVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
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                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVIFLYLFIVKPLVPR---ILESLNSSRNPQETSILSKIENDLLDDLDINCLNIFNGSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYKELSQVTIQRVLFMLSSIYHPQNEYCIAVGENSAPIFQNLLKELSNCFSNIHF-MKRP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHKD--AIMVER----LIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASKLE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNQLRIVNSRSI-----EDKLLYSTDRCQTLKSLFRFNKVPLSPEEESFPLSYGLL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLAEKLEEQQR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTDGWRYYISRDQIWSKPNCHNYMKAGSCVFGIGDVPRLLKSKALVAHKFYLKSEPEAYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLSSSSIPQQLLEFLRNTGIADEGFWGTLFGNKNLFDIPGSLNFKEWISYKNNVETNLTY 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIFNNSIVQDFFAWSKDTYSPDEHFWATLI----RVPGIPGEISRSAQDVSDLQSKTRLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDWGSHEIINSAYDCLEFLSHLKSDWRYFQYLSGVDIPLKTNLEMVQILKHLNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVEYAHISRLQADLNCLSDLLKSSIQWKYYINLCGQDFPLKSNFELVSELKKLNGANMLE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KWNYY----EGFFYPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPILIK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TANVEIK--PYQYQRL--RGKNETQSP---LPLFKSSLSSLIPREAAN 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
                                                                                                                                                                                                        1-425 <WI2>
                                                                                                                                                                                                                                                                                                                                                                      1-425 <WIL>
                                                                                             ; 117/3;
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     Conservative
                                                                                                                                                                                                                                                                                                                                                    EMBL: 283102; PIDN: CAB05469.1; GSPDB: GN00019; CESP: C54C8.11
                                                                                               161/3; 195/3; 237/3; 266/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.6%;
                         13.5%;
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Pred. No. 2e-16;
Score 323; DB 2, -
Pred. No. 3,1e-16;
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                                                                                               295/1; 313/3;
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                                        Length
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       Indels
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         88;
                                                                                                 355/1;
                                                                                                                                                                                        CESP: C54C8.11
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submitted to the EMBL Data Library, April 1996
A;Reference number: Z19397
A;Accession: T21261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F22D6.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Introns: 62/3; 92/2;
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:271262; PIDN:CAA95816.1; GSPDB:GN00019; CESP:F22D6.12 A;Experimental source: clone F22D6
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A; Residues: 1-454 <WIL>
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g
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WIHKNYRTRGKLGKYGENQKIDNGYYVSRYQQYVNRAPVKCKGYYYRLSCVFGVYDLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDVSDL-QSKTRLVKW-----NYYEGFFYP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F--SRKSANFMVNSEKVLEQIDFLRGTTCADESLWATIAGNPKVIKFSELPMPGGFDAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALNG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --FIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KMFDGDPVSLA-----RGALFKFDDREILAQILKLSGQENAQCAEFQKIFGFFQEPTSQ
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                                                                                                       SKEEKSFPIAYSLVVHKDA---
                                                                                                                                             LLDNMEINCSNIL--KGYKTNEKLDIMHLDII---EEQLFSCINKCQTLKTLFRFNINPM 107
                                                                                                                                                                        ---RYEVNCSGIYEQEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLV 124
                                                                                                                                                                                                                  FKTSLIIAIFFLFI-----YFSVESLFPRKQ----EDKNVSKQFLKSICTTASDSY 52
                                                                                                                                                                                                                                                   FKHTLQQKVFILFLTLWLLSLLKLLNVRRLFPQKDIYLVEYSLSTSPFVRNRYTHVKDEV 67
NSAPIFONLLREVSTCFSNVHF-MKRPPISWGSHEIIDSVYDCLEFLSHLETDWRYFQYL
                                  KAPDTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINL
                                                                     SAEEKHFPLSYGMLVYKDLPQVTPARMFIKLHFLEINLQVLFLLSSIYHPQNEYCIAVGE
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                              190/3; 266/3; 291/3; 412/3
                                                                                                                                                                                                                                                                                                       13.2%;
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                                                                                                                                                                                                                                                                                       79;
                                                                                                                                                                                                                                                                                     Score 315.5; DB 2;
Pred. No. 1.2e-15;
9; Mismatches 190;
                                                                                                       -IMVERLIHAIYNQHNIYCIHYDR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SCTGSHLRSVCIYGAAELRW 400
                                                                                                                                                                                                                                                                                                                        Length 454;
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 226
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                                    226
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hypothetical protein T15D6.2 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t-C;Accession: T24929
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A; Introns: 45/3; 75/2; 111/3; 151/3; 227/3; 252/3; 296/2; 359/3
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A;Residues: 1-401 <WIL>
A;Cross-references: EMBL:Z83125; PIDN:CAB05620.1; GSPDB:GN00019; CESP:T15D6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data A; Reference number: Z19956 A; Accession: T24929
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Best Local S
Matches 86
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341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 THYKDEVRYEVNCSGIYEOEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 23.4 les 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVPRLRTSKALVAHKFYLKSEPEAYFCL - - - LKEHHR 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQQR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQFNISGSINSKDWMEYRDNQNNIFNPTDGWSYYISRDQIWDPELCKNYMKDDSCVFGIG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GIPGEI-SRSAQDVSDLQSK--TRLVKWNYY---EGFFYPSCTGSHLR-SVCIYGAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --NESP---LPLFKSSLSATIPRKAANQLASSNTARKLLEFLWNTETADEGFWGTLFGNK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVDIPLKTNLEMVQILKHLNGTSNVEIT - - - NYQQARLTGKNE - - -
                                                                                                                                                                    GSAYFYLSQAFYKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPG----IPGEISRSAQ 357
                                                                                                                                                                                                                    RILKSLNGTANVEIKVYENRRL---
                                                                                                                                                                                                                                                      SELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFV 300
                                                                                                                                                                                                                                                                                         DCFPN----KRPPITWGSYEIINSVYDCLKFLSHLKSNWKYFQYLSGVDIPLKTNLEMV
                                                                                                                                                                                                                                                                                                                          KCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELV 240
PEAYFCL
                                 PILIKCL
                                                                                                                                          SSLSSLIPRKAANYLASSSIPQQLLEFLRNTWVADEGFWGTLFGNKGLFDVPGSLN----
                                                                                                                                                                                                                                                                                                                                                                 EVPLSEEEARFPLSYGLLVYKELSQVLFMLSSIYQPQNEYCIAVGENSASTFLILLEELS 146
                                                                                                       DVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVD
347
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                                                                      FEEHQIWFESGCHNHMKDGSCVFGIGDVSNLLQAKALVAHKLYLTSE 340
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%; Pred. No. 2.8e-14;
68; Mismatches 157
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RESULT T22188

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hypothetical protein F44F4.6 - Caenorhabditis elega
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T22188
                                                 A; Molecule type: DNA
A; Residues: 1-402 <WIL>
A; Cross-references: EMB
                                                                                                                                                          C;Accession: T24930
R;Dobson, R.
submitted to the EMBL Data Library,
                                                                                                                                                                                                                  hypothetical protein T15D6.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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A; Introns: 57/2; 105/2; 185/3; 261/3; 319/1; 370/1; 412/3
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A; Residues: 1-472 <WIL>
A; Cross-references: EMBL: 237092; PIDN: CAA85457.1;
A; Experimental source: clone F44F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: Z19528
A; Accession: T22188
             A; Experimental source: C; Genetics:
                                                                                                                        A; Reference number: 219956
A; Accession: T24930
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                                                                                                     A; Status: preliminary; translated
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Best Local
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CESP: T15D6.3
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                                                                                                                                                                                                                                                                                                                                                                                  ANKFDSKVDPILIKCLAEKLEEQQ------RDWITLPSEKLFMDRNLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103;
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                                 EMBL: 283125; P
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    Caenorhabditis elegans

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                                                   PIDN:CAB05621.1; GSPDB:GN00019; CESP:T15D6
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Pred. No. 4.9e-14;
Nismatches 184; Indels 102;
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                                                                                                                                                              November 1996
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hypothetical protein T09E11.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T24742
R;MCLay, K.
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                                                                                                                                                                                                  A;Map position: 1
A;Introns: 39/1; 78/3; 204/1; 291/1; 338/3; 371/3; 417/3
C;Superfamily: Caenorhabditis elegans hypothetical protein H41C03
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A; Introns: 55/3; 85/2;
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                                               Дb
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                                                                                                                                                                                                                                                   A;Cross-references: EMBL:281147; PIDN:CAB03536.1; GSPDB:GN00019; A;Experimental source: Clone T09E11 C;Genetics: A;Gene: CESP:T09E11.9
                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-459 <WIL>
                                                                                                                                                                                                                                                                                                                                                                      A; Reference number:
A; Accession: T24742
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Best Local :
                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263
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                  101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 VFILELTLWLLSLLKLLNVRRLFPQKDIYLVEYSLSTSPFVRNRYTHVKDEVRYEVNCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                 25
                                                                                43 IYLVEYSLSTSPFVRNRYTHVKDEVRYEVNCSGIY--EQEPLEIGKSLEIRRRDIIDLED 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYYLMFS-SKSLFGRN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -WVESECHNYMKD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KW-----NYYEGFFYPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPILIKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSSVPQQLLEFLRTTWVADEGFWGTLFGNKDLFNVPGSFNFNDPLTNGWGNYVSRHQL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNNSIVQDEFAWSKDTYSPDEHFWAT-----LIRVPGIPGEISRSAQDVSDLQSKTRLV 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVKYI 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWGSFEIINSVYGCLEFLSHLKSDWKYFQYLSGVDIPLKTNLEMVRILKRLNG-----TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYAHISRLQADLNCLSDLLKSSIQWKYYINLCGQDFPLKSNFELVSELKKLNGANMLETV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIFIASKLEAV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILQGFKNE -- NTLELINTKMI -- - ENKMWNSTDRCQTLTSMFRFNKVPLSEEEARFPLSF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IYEQEPLEIGKSLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVSKEEKSFPIAY 135
                                                                                                                      106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121/3; 161/3; 237/3; 262/3
                                                                                                                                   10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%;
24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          Library,
                --DDVVAMTSDCDIYQTLRGYAQKLVSKEEKSFP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RS-CVFGIGDVPNLMKSRALVAHKLYIESEPEAFFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69,
                                                                                                                                   Score 245; DB 2;
Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 275; DB 2; Pred. No. 9.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---LNGKNKTESP---LPLFKSSLSSLIPRKAANYL
                                                                                                                                                                                                                                                                                                                                                                                                            October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                      Mismatches
                                               -EQNSYALYNLRNENYQREAIINELRRDFAKIES 72
2:
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                                                                                                                                                   Length
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Fri

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RESULT 10
T25382
hypothetical protein T27F6.1 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Apate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T25382
R;Dobson, R
R;Dobson, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Дb
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A;Experimental source: clone T27F6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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A;Introns: 80/3; 191/1; 278/1; 325/3; 365/2; 407/3
C;Superfamily: Caenorhabditis elegans hypothetical protein H41C03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뫄
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Best Local 9
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nes 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 FILFLTLWLLSLLKLLNVRRLFPQKDIYLVEYSLSTSPFVRNRYTHVKDEVRYEVNCSGI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMAACLPNVLLLPDQEPIDSNGHNVNLAHLNCLRALINKP-GWNYAMLLQNHDLLTKSVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPEDNSIIECTAELLYNRTFMGQNDH---PLEEEYY-KNMVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKVDPILIKCLAEKLEEQ - - - - QRDWITLPSEKLEMDRNLTTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFVGSAYFVLSQAFVKYIFNNSIVQDFF-AWSKDTYSPDEHFWATL--IRVPGIPGEISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLR-SVCIYGAAELRWLIKDGHWFANKFD 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSKGGVQGSMSRAAVDWMTRKVNLSTYIDQWNQGRWGVDEMLISSLQISAFLGMPGHF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEQVYEWLGGANDVELL-PEAQRIDEENFKWD----PRSIKMFPDESKVDETTLNEKIK
                                                                                                                                                                                                                                             CEAVMDRILSRDHVLRPLENGVAFARVVYMDYELIEKHVEMSYHPQNSFCFAIDKKAAKE
AILLQNHDLITKSVYELEKIFNWLGGANDV-AIRPELGRLDK----
                                                           VINLCGODFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                  YEQEPLEIGKSLEIRRRDIIDLEDDDV----VAMTSDCDIYQTLRG-YAQKLVSKEEKSFP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIL-----LVALLCTLN------WFLYNYQV-----YRNHYWSYTQNSSFQEDIAKF
                                                                                                                             FKERMQAMASCLPNVLLLPGRFFKNPIHDLSVDSHGHNTNL-AHYNCLRALINKP-GWNY
                                                                                                                                                                                                                                                                                                                                                                   YPTSNKDY---FVYRRRP----ETENVNCGQVLAGDTAYLKTVTGEYRIKIAENESLNMS
                                                                                                                                                                                 FKVAMNNLAKCFSNIFI------ASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----IAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMN
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                                                                                                                                                                                                                                                                                                    --IAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 229.5; DB 2;
Pred. No. 2.5e-09;
8; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459
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         -KHFKWDPMSLK
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C; Accessi
R; Harris,
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                 δÃ
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A;Experimental source: clone R07B7
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A; Map position: 5
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A; Residues: 1-489 <WIL>
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Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VKDEVRYEVNCSGIYEQEPLEIGKSLEIRRDIID-----LEDDDVVAMTSDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAT--LIRVPGIPGEIS-RSAODVSDLQSKTRLVKWNYYEGFFYPSCTGSHLR-SVCIYG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFRNESEIDPVILNTTLKFAKGAVQSSLSRAAVDWMTRTVDLTTFIDQWNHGTYGVDEQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRTNISKEAP---PHNIQIFVGSAYFVLSQAFVKYIFNNSIVQDFF-AWSKDTYSPDEHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TILKLSEMSATRYKRLTDIDLDADINTARVSLQDNGKNSPILRTRSQEKPRKRNITKWMD
                                                                NYLGLEGOMESNCTRNHNDI--LTRMTHWDFSGPNGFDKECHSKWKRHGICIMGVEYMNE 407
                                                                                             RVPGIPGEI-SRSAQDVSDLQSKTRLVKWNYY-EGFFYPSCTGSHLR-SVCIYGAAELRW 400
                                                                                                                                 PNEILNRNLIVRKSLNEVIVSKVFVKSMFEKLNMDIIIKLFD-DNDYYGVDEMLVQTLYE
                                                                                                                                                                 SKEAPPHNIQIFVGSAYFVLSQAFVKYIF---NNSIVQDFFAWSKDTYSPDEHFWATLI
                                                                                                                                                                                                   DLIIKTPYQLSDISESLNYTSIM------GFDHGFSYRYNTKAKWTPAGMKLFKIETGV
                                                                                                                                                                                                                                   DFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRR--VPYEYVKLPIRTNI
                                                                                                                                                                                                                                                                   DRLKESVRIMSSCFTNVVVVLGKEYSLNSGGHGQDPAHFDCLKTILDR--KWDHAIILQNF
                                                                                                                                                                                                                                                                                                    DTFKVAMNNLAKCFSNIFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQ
                                                                                                                                                                                                                                                                                                                                  PSIKNRIYG----DMPSFRPLKRPIAFVRTIYKIYELQEALLSISYHPDNVFCFVMDSKST
                                                                                                                                                                                                                                                                                                                                                                 -DIYOTLRGYAQKLVSKEEKSEPIAYSLVVHKDAIMVERLIHAIYNOHNIYCIHYDRKAP 169
                                                                                                                                                                                                                                                                                                                                                                                                      NYFTADESQF-LNCSEMIK-------NNKDVIELYVNNGRMKLDNERLFELPMDC
                                LIKDGHWFANKFDSKYDPILIKCLAEKL-----EEQQRDWIT
 LIKSQQVIANKVMATFDFGTIACMREMIKRNTAGETPNTQWLT
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Pred. No. 1.3e-08;
"""matches 209;
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RESULT T32137

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hypothetical protein R07C3.3 - Caenorhabditis elegans
(;Species: Caenorhabditis elegans
C;Date: 29-oct_1999 #sequence_revision 29-oct-1999 #text_change 20-Jun-2000
C;Accession: T32137
R;Lamar, B; Kramer, J.
Submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid R07C3.
                                                                             A; Reference number: Z19
A; Accession: T21566
A; Status: preliminary;
                                                                                                                           submitted to the EMBL Data Library, A; Reference number: 219442
                                                                                                                                                                                             hypothetical protein F30A10.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T21566
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A;Introns: 18/1; 78/3; 189/1; 276/1; 319/3; 359/2; C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AF016686; PIDN:AAB66233.1; GSPDB:GN00020; CESP:R07C3.3
A;Experimental source: strain Bristol N2; clone R07C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-470 <LAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: The sequence of A; Reference number: Z21125 A; Accession: T32137
A; Molecule type: DNA 4, Residues: 1-486 <WIL> A; Residues: 1-486 <WIL> A; Cross-references: EMBL: Z81072; PIDN: CAB03022.1; GSPDB: GN00019; CESP: F30A10.4 A; Experimental source: clone F30A10
                                                                                                                                                                        R; Barlow,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRAAHCATGTVRHDICIFGIEDFRAI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEIRRRDII--DLEDDDVVAMTSDCDIYQTLRGYAQKLVSKEEKSFPI-----AYSLVVH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSRNSSYLDPKLSVDRELAVYKRITEALRTVDRSCEEQGFYCKRPETQHVDCGRVLVGDK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPOKDIYL-VEYSLSTSPFVRNRYTHVKDEVRYEVNCSGIYEQEP------LEIGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFFYPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPIL------IKCLA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLERETYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFVGSAYFVLSQAFVKYIFNNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELKKLNGANMLETVKPPNS
                                                                                                                                                                                                                                                                                                                                                                         ELL--HNRTYLGQVDQKI--EKNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSIFIDQWNQTDYGADEQFISTFQMSPDLKMPGHFTNECIHNDTAIVTISRLARWVPIYL
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Pred. No. 1.4e-08;
3; Mismatches 207;
                                                                                      from
                                                                                                                                                                                                                                                                                                                                                                         435
                                                                                                                                                     October 1996
                                                                                      GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SKF-----PILNMLPAFDYSIIECTA 415
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protein H41C03.3
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A;Gene: CESP:F30A10.4
A;Map position: 1
A;Introns: 19/3; 59/3;
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A;Introns: 48/1; 94/3; 117/3; 220/1; 307/1; 354/3; 394/2; 4
C;Superfamily: Caenorhabditis elegans hypothetical protein
                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-472 <LAT>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, July 1998 A; Description: The sequence of C. elegans cost
                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
C;Accession: T33384
R;Latteille, P.; Kramer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein H41C03.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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                                                                                                                                                                                                              A; Gene: CESP: H41C03.3
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Matches 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SESRY-LNCARLIDGDVESIDTYVNNGR----MKLDEEKLFQLSMDCDSIQ--NRIFRDMP
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                                FLTLWILSLLKLLNVRRLF----PQKDIYLVEYSLSTSPFVRNRYTHVKDEVRYEVN--- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLDGQMESNC-TVAKEDILTROTHWHLEQSDGLYQDCKSKWLRHSICVIGVEFLQELSKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILNYTSIMGEDYGFTSRYRTFEDWTPAGMKL----FKNE-QSVPLEILHKKLKIRKSLNE
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FKFIWILLFLAVCFYAYYLWIFNPKKGIY---DPLTTDKQNPMTYEQVVNDLRNEIDQRN
                                                                      90;
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ce: strain Bristol N2; clone H41C03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93/2; 248/3; 300/1; 348/3; 385/2; 429/1
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Pred. No. 1.
                                                                                        Score 203.5; DB 2; Pred. No. 2.2e-07;
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n H41C03.3
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                                                                          16;
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A;Mclecule type: DNA A;Residues: 1-753 <wil> A;Residues: 1-753 <wil> A;Cross-references: EMBL:Z81147; PIDN:CAB03539.1; GSPDB:GN00019; CESP:T09E1 A;Experimental source: clone T09E11 C;Genetics: C;Genetics: A;Gene: CESP:T09E11.6 A;Map position: 1 A;Introns: 34/2; 54/2; 191/3; 275/3; 315/3; 359/3; 380/3; 403/3; 426/3; 530.</wil></wil>
ESP:T09E

Search completed: August 2, 2001, 14:45:50 Job time: 136 sec

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Sequence:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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  August 2, 2001, 14:45:20 ; Search time 16.71 Seconds (without alignments) 928.650 Million cell updates/sec
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    FGR2_HUMAN
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YCF2_FINH
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BACLE
VOO1_VACCC
CEK3_CHICK
A23D_HOKAN
FETX_CLOTE
GAAP_HUMAN
YOB6_CAEELPJ
D73B_MYCGE
DNAA_BUCAP
DF3B_MYCGE
CH1_HUMAN
CLH_BOVIN
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Q06430 homo sapien
Q58454 methanococc
P34761 saccharomyc
Q01742 homo sapien
P21802 homo sapien
P21803 mus musculu
P41653 pinus thunb
P09976 nicotiana t
C088007 bacilius li
P21093 vaccinia vi
P18461 gallus gall
Q24093 drosophila
P04958 clostridium
C00591 homo sapien
C00595 caenorhabdi
C15457 homo sapien
C09259 caenorhabdi
C15474 mycoplasma
P29434 buchnera ap
P23116 mus musculu
C00610 homo sapien
P47247 buchnera ap
P33116 mus musculu
C00610 homo sapien
P4951 bos taurus
P11442 rattus norv
C66006 b bacitraci
P51381 porphyra pu
P38110 saccharomyc
  Q9xs28
Q60270
P52304
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Q09324 mus musculi
Q92180 bos taurus
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se by non-profit institutions as long as its odified and this statement is not removed. Usacodified and this statement is not removed. Usacodified an email to licensedisb-sib.ch).  r send an email to licensedisb-sib.ch).  MBL: M97347; AAA35919.1;  MBL: L41415; AAA95661.1;  IR; A46293; A46293.  IN; 600391;  ransferase; Glycosyltransferase; Transmembrane;	D-GLOCUSARINIL- RESSED IN ACTI RESSED IN ACTI YME (IGNT).  It is produce oinformatics of other ear	RN [2]  RN [2]  RP SEQUENCE FROM N.A.  RC TISSUE-Placenta;  RC TISSUE-Placenta;  RC TISSUE-Placenta;  RC TISSUE-Placenta;  RE Hierhizen M.F.A., Maemura K., Kudo S., Fukuda M.;  RA Bierhizen M.F.A., Maemura M., Kudo S., Fukuda M.;  RA Bierhizen M.F.A., Maemura M., Kudo S., Fukuda M.;  RA Bierhizen M.F.A., Maemura M., Kudo S., Fukuda M.;  RA Bierhizen M.F.A., Maemura M., Kudo S., Fukuda M.;  RA Bierhizen M.F.A., Maemura M.,	ding UDP-GlcNAc ta 1-6GlcNAc tr polyoma large 326-9330(1992).	iata; Vertebrata rrhini; Hominida	Q02742; Q02742; Q1-JUN-1994 (Rel. 29, Created) Q1-JUN-1994 (Rel. 29, Last sequence update) Q1-NOV-1997 (Rel. 35, Last annotation update) BETA-1,3-GALACTOSYL-G-GLYCOSYL-GLYCOPROTEIN BETA-1 ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE (COREZ-GLCNAC-TRANSFERASE) (CZGNT) (CORE 2 GNT).	428 AA.	LIGNMENTS	NAN NASAN AFA
ant is in no wa and for commercia isb-sib.ch/announce	GI.  C-LYMPHOC  C-LYMP	COD OF	DP-GlcNAc:Gal beta GlcNAc transferase by gene ma large tumor antigen."; 30(1992).	a; Euteleostomi; ae; Homo.	(1,6-N- RE 2 BRANCHING ENZYME)		0103	051498 borrelia bu 002740 bos taurus Q14152 homo sapien P121249 onchocerca P47520 mycoplasma P38903 saccharomyc Q04956 plasmodium Q58030 methanococc P05728 euglana gra P47988 saccharomyc D15917 bactilus an

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G6NT_M
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Best Loc
Matches
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SEQUENCE
                                                                                                                              G6NT_MOUSE STANDARD; PRT; 428 AA. Q09324; Q09324; Q1-NOV-1995 (Rel. 32, Created) Q1-NOV-1995 (Rel. 32, Last sequence update) Q1-NOV-1997 (Rel. 35, Last annotation update) BETA-1,3-GALACTOSYL-O-GLYCOSYL-GLYCOPROTEIN BHACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE2-GLCNAC-TRANSFERASE) (C2GNT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Golgi
DOMAIN
                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                        GCNT1
                                                             STRAIN-DBA/2;
                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                 YFVLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIPGEISRSAQ-DVSDL
                                                                                                                                                                                                                                                                                                                                          LMGENNLETERMPSHKEERW
                                                                                                                                                                                                                                                                                                                                                            LNGANMLETVKPPNSKLERFTYHHELRRVPYEYV--KLPIRTNISKEAPPHNIQIFVGSA
                                                                                                                                                                                                                                                                                                                                                                                                                KEEAEFPIAYSIVVHHKIEMLDRLLRAIYMPQNFYCVHVDTKSEDSYLAAVMGIASCFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                KEEKSFPIAYSLYVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCTKYLQGDVNEIQKVKLEILTVKFKKRP--RWTPDDYINMTSDCSSFIKRRKYIVEPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCSGIYEQEPLEIGK-----SLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLRTLLRRRLFSYPTKYYFMVLVLSLITFSVLR---IHQKPEFVSVRHLELAGENPSSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187;
                                                                                                                                                                                                                                                      PILIKCLAEKLEEQ
                                                                                                                                                                                                                                                                       QAVARFVKWQYFEGDVSKGAPYPPCDGVHVRSVCIFGAGDLNWMLRKHHLFANKFDVDVD
                                                                                                                                                                                                                                                                                                         YFVVSREYVGYVLQNEKIQKLMEWAQDTYSPDEYLWATIQRIPEVPGSLPASHKYDLSDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stack;
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52
58
95
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                                                                                                               (Mouse)
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52
58
95
49784
                                                                                              Chordata;
Rodentia;
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43.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUMENAL, CÁTALYTIC (POTENTIAL).

**LINKED (GLCNAC. . .) (POTENTIAL)

**N-LINKED (GLCNAC. . . .) (POTENTIAL)

**N-LINKED (GLCNAC. . . .) (POTENTIAL)

**TOPECEB51DA00A60 CRC64;
                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                           -KKRYEVVNGKL-TNTGTVKMLPPLETPLFSGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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DR (TYPE-II N
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                                                                                                                                       BETA-1,
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                                                                                                                                        ,6-N-
2 BRANCHING
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                                                                                              Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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                                                                                               Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΕV
                                                                                                                                          ENZYME)
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STEPPER WWW.
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Matches 183
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
092180;
01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
01.NOV-1997 (Rel. 35, Last annotation update)
01.NOV-1997 (Rel. 35, Last annotation update)
BETA-1,3-GALACTOSYL-O-GLYCOSYL-GLYCOSYCTEIN BETA-1,
ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE
(COREZ-GLCNAC-TRANSFERASE) (C2GNT) (CORE 2 GNT).
GCNT1.
                                                                                                                        BOVIN
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Golgi stack;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: GLYCOSYLATION: TYPE II MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
SIMILARITY: TO I-BRANCHING ENZYME (IGNT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; U19265; AAA60948.1; MGI:95676; Gcntl.
                                                                                                                                                                                                                                                                                                                                                                   LNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHNIQIFVGSAYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCSGIYEQEPLEIGK-----SLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLRNLFRRRLFSCPTKYYFMLLVLSLITFSVLR---IHQKPEFFSVRHLELAGDDPYSNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
183; Conser
                                                                                                            BOVIN
                                                                                                                                                                              AIQCLDEHLRRK
                                                                                                                                                                                                        LIKCLAEKLEEQ
                                                                                                                                                                                                                                                                                                               VLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIPGEI-SRSAQDVSDLQS
                                                                                                                                                                                                                                                                                                                                            STGENNLETEKMPPNKEERWK - - -
                                                                                                                                                                                                                                                                                                                                                                                                VFVASQLESVVYASWTRVKADLNCMKDLYRMNANWKYLINLCGMDFPIKTNLEIVRKLKC
                                                                                                                                                                                                                                                                                                                                                                                                              IFIASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYYINLCGQDFPLKSNFELVSELKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEEVGFPIAYSIVVHHKIEMLDRLLRAIYMPQNFYCIHVDRKAEESFLAAVQGIASCFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCTKILQGDPEEIQKVKLEILTVQFKKRP--RWTPHDYINMTRDCASFIRTRKYIVEPLT
                                                                                                                                                                                                                                  KTRLVKWNYYEGFF-----YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPI
                                                                                                                                                                                                                                                                                       VVTREYVGYVLENENIQKLMEWAQDTYSPDEFLWATIQRIPEVPGSFPSSNKYDLSDMNA
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58
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428
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Glycoprotein.
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                                                                                                            STANDARD;
                                                                                                                                                                                421
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58
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49849
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SIGNAL-ANCHOR (TYPE-II MEMBRANE (POTENTIAL).

LUMENAL, CATALLYTIC (POTENTIAL).

LUMENAL, GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-SIFFD2517B27AAE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 848.5;
Pred. No. 2.4e
72; Mismatches
                                                                                                                                                                                                                                                                                                                                             --KRYAVVDGKL-TNTGIVKAPPPLKTPLFSGSAYF
                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                              427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
)R (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4e-54;
                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal-anchor;
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                              ,6-N-
2 BRANCHING
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9;
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                               ENZYME)
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Query Match
Best Local S
Matches 185
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: FORMS CRITICAL BRANCHES IN O-GLYCANS.

-i- CAPALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL-1,3-N-ACETYL-D-GALACTOSAMINYL-R = UDP + BETA-D-GALACTOSYL-1,3-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,3-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GALACTOSYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5)-N-ACETYL-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETYL-BETA-D-GLUCOSAMINYL-1,5-(N-ACETYL-BETA-D-GLUCOSAMINYL-1,5-(N-
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE SIMILARITY: TO I-BRANCHING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALACTOSAMINYL-R.
PATHWAY: GLYCOSYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLRKLWRRKLFSFPTKYYFLFLAFSVVTFTVLR---IHQKTEFVNFGHLELFEENPSSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLKLLNVRRL--FPQKDIYL-VEYSLSTSPFVRNRYTHVKDE-VRY------EV 71
                                                                                                        KTRLVKWNYYEGFF-----YPSCTGSHLRSVCIYGAAELRWLIKDGHWFANKFDSKVDPI
                                                                                                                                                                                                                                                                                                                                   GENNLETEKMPSHKKERWKKH-----YEVVNGKL-TNMGTDKIHPPLETPLFSGSAHF
                                                                                                                                                                                                                                                                                                                                                                                                GANMLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNI--SKEAPPHNIQIFVGSAYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASQLESVYYASWSRVQADLNCMQDLYQMNAGWKYLINLCGMDFPIKTNLEIVRKLKLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IASKLEAVEYAHISRLQADLNCLSDLLKSSIQWKYVINLCGQDFPLKSNFELVSELKKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAGFPIAYSIVVHHKIEMLDRLLRAIYMPQNFYCIHVDAKSEKSFLAAAVGIASCFSNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCTKILQGDVDEIQKVKLESLTVKFKKRARWTNYDYINMTGDCASFIKKRKYITEPLSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCSGIYEQEPLEIGK----SLEIRRRDIIDLEDDDVVAMTSDCDIYQTLRGYAQKLVSKE 127
                                                                IARFVKWQYFEGDVSKGAPYPPCS-VHVRSVCVFGAGDLNWLLHVHHLFANKFDTDIDLF
                                                                                                                                                                                                  VVSREYVEYVLQNQNIQKFMEWAKDTYSPDEYLWATIQRIPEVPGSLSLSYKYDTSDMQA
                                                                                                                                                                                                                                                       VLSQAFVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIPGEISRSAQ-DVSDLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCIHYDRKAPDTFKVAMNNLAKCFSNIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA83244.1;
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Pred. No. 9.
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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LUMENAL, CATALYTIC (POTENTIAL)
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ENZYME (IGNT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnet A.D., Fukuda M.;
"Expression of the large I antigen forming be acetylglucosaminyltransferase in various tiss Glycobiology 7:285-295(1997).
-!- FUNCTION: BRANCHING ENZYME THAT CONVERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PATHWAY: GLYCOSYLATION.
-i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI
-i- SIMILARITY: TO CORE 2 BRANCHING ENZYME (C2GNT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE
(EC 2.4.1.150) (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING IGNT) (LARGE I ANTIGEN-FORMING BETA-1,6-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCNT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1100870; Gcnt2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97280061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLGLUCOSAMINYLTRANSFERASE).
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CAPALYTIC ACTIVITY: UDP'N'-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSY -1,4-N'-ACETYL-D-GLUCOSAMINYL-R.

GLUCOSAMINYL-1,6-BETA-D-GALACTOSYL-1,4-N'-ACETYL-D-GLUCOSAMINYL-R.
                                               VVAMTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKDAIMVERLIHAIYNQHNIYCI
                                                                                                                                              IYLVEYSLSTSPFVRNRYTHVKDEVRYEVNCSGIYEQEPLEIGKSLEIRRRDIIDLEDDD
                                                                                                   VCVVSYVLSFGGDQSYQKLNISDSVRLSQVCSSFID-
MIHEKPSCTEYVTQSHYITAPLSQEEGDFPLAYVMVIHHNFDTFARLFRAIFMPQNIYCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ferase; Glycosyltrans stack; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U68182; AAB39621.1;
                                                                                                                                                                                                al Similarity 40.0
156; Conservative
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                                                                                                                                                                                                                       30.6%;
                                                                                                                                                                                                                                                                                                                         WW.
                                                                                                                                                                                             k; Score 730.5;k; Pred. No. 7.6e51; Mismatches
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N-LINKED (GLCNAC...) (POTENT:
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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various tissues of ad
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                                                                                                                                                                                                  es 160;
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) (POTENTIAL).
) (POTENTIAL).
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MBL outstation -
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BGIB_HUMAN
Q06430;
                                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta;

MEDLINE=96078409; PubMed=7579796;

Bierhuizen M.F.A., Maemura K., Kudo S., Fukuda M.;

"Genomic organization of core 2 and I branching beta-1,6-N-acetylglucosaminyltransferases. Implication for evolution of the beta-1,6-N-acetylglucosaminyltransferase gene family.";

Glycobiology 5:417-425(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OUR-1994 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
N-ACETYLLACTOSAMINIDE BETA-1,6.N-ACETYLGLUCOSAMINYLTRANSFERASE
(EC 2.4.1.150) (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING)
                                                                                                                                                                                                                                Sasaki K., Kurata-Miura K., Ujita M., Sekine S., Nishi T., Fukuda M.; Texpression cloning of DNA encoding a acetylglucosaminyltransferase that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93194065; PubMed=8449405;
Bierhuizen M.F.A., Mattei M.-G., Fukuda M.;
"Expression of the developmental I antigen by a cloned human cDN
encoding a member of a beta-1,6-N-acetylglucosaminyltransferase
                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY.
MEDLINE=98070745; PubMed=9405606;
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Mammalia; Eutheria;
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                                                               tyllactosamine synthesis.";

c. Natl. Acad. Sci. U.S.A. 94:14294-14299(1997).

c. Natl. The Development and Maturation of Ervithroid Cells.

c. Natl. The Development and Maturation of Ervithroid Cells.

c. OATILITY: UDP-ACETYL-D-GLUCOSAMINE + BETA-D-GALACTOSYL-1,4-N-ACETYL-BETA-D-GALACTOSYL-1,5-BETA-D-GALACTOSYL-1,4-N-ACETYL-D-GLUCOSAMINYL-R.
                 SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI TISSUE SPECIFICITY: IN THE ADULT, HIGHLY EXPRESSED IN
                                                   PATHWAY: GLYCOSYLATION.
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SMALL
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EMBL; L19550; CAA79610.1; -.
EMBL; L41607; AAA99832.1; -.
EMBL; L41605; AAA99832.1; JOIN
EMBL; L41606; AAA99832.1; JOIN
EMBL; L41606; AAA99832.1; JOIN
EMBL; L41606; AAA99832.1; JOIN
EMBL; A46297; A46297.
 YA54_METJA
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL
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MEDLINE=96337999; PubMed=8688087;

Buit C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Button G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (see http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE UDP-GLUCOSE/GDP-MANNOSE DEHYDROGENASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus.
NCBI_TaxID=2190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U67548; AAB99056.1; TIGR; MJ1054; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                  YNOHNI-----SNIFIASKLEAVEY 197
                                                                                                                                                                                                                                                                                                  E-----ILDKY----GSKNRLFTAKSKSTTIPYKIKIDKDFARLIGYYLSEGWISKD
                                                                                                                                                                                                                                                                                                                               DDDVVAMTSDCDIYQTLRGYAQKLVSKEEKSFPIAYSLVVHKD-----AIMVERLIHAI 153
                                                                                                                                                                                                                                                                                                                                                                 EIDILE-ELSKTDLIEKVWIHNKDLATNEFNIIKPYLSNKYPHDVKRNGTIRAKDILPIK
             LQSKT-
                                                                                                                                                                        ENI--LNCGINCYNKNIPPQMFNAKEEIKWEF-----LKGLFRGDGGIVRLNNNK
                                                                                                                                                                                                     AHISRLQADLNCLSDLL-----
                                                                                                                                                                                                                                     YGRNGVVRKRIGLCFGIHEEEYINDV-KNILNKLGIKYIEKIKDGSHSILISSKILAYVF
                                                                          FVKYIFNNSIVQDFFAWSKDTYSPDEHFWATLIRVPGIP-----
                                                                                                                                        MLETYKPPNSKLERFTYHHELRRVPYEYYKLPIRTNISKEAPPHNIQIFVGSAYFVLSQA
                                             -VKKCYNN-----KST----TMAYIIRINGLEQVKKIGELFGKKWENYKDIAE
                                                                                                          NLNIEFAT
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-RLVKWNYYEGFFYPSCTGSHLRSVCIYGAAELRWLIK
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Pred. No. 0.
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RESULT 7
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MEDLINE=95242839; pubMed=7725799;

Tonniaux J. L., Coster F., Purnelle B., Goffeau A.;

Tonniaux J. L., Coster F., Purnelle B., Goffeau A.;

Tonniaux J. L., Coster F., Purnelle B., Goffeau A.;

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P34761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
Nash R.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1993)
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WHI3 OR YNL197C OR N1382.
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SEQUENCE
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EMBL; X78898; CAA55511.1; -.
EMBL; Z71473; CAA96092.1; -.
HSSP; P09012; 2U1A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD; S0005141; WHI3.
InterPro; IPR000504; -
Pfam; PF00076; rrm; 1.
PROSITE; PS50102; RRM;
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                                                                                                                                                                                                                                                                        RGYAQKLVSKEEKSFPIAYSLVVHKDAI--MVERLIHAIYNQHNIYCIHYDRKAPDTFKV 174
                                            AINYAVILNSKNELFGPSFPNKTTVEIIDDTTKNLVSFPSSAIFNDTSRLNKSN--SGMK
                                                                                                                                       KLSNVAKDITLRECYAIFALAEGVKSIELQKKNSSSSITSASLEDENDIFIIARFELLNL
                                                                                                                                                                                      AMNNLAK - - - -
                                                                                                                                                                                                                                RGSASGELYLNDTNSPLAISSMLNTLALGSMPQDIASSNISNH------DNNIKGSYSL 104
  PPN - - SKLERFTY -
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661 AA;
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Pred. No. 1.6;
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HHELRRYPYEYVKLPIRTNISKEAPPHNIQIFYGSAY
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InterPro; IPR001245; -.
InterPro; IPR0013006; -.
InterPro; IPR0003006; -.
Pfam; PF00047; ig; 2:
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR SIMILARITY:
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o cDNAs encoding novel human For receptor.";
him. Biophys. Acta 1089:244-246 (1991).
FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIB
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PS00109; PROTEIN_KINASE_TYR; 1.
PS50011; PROTEIN_KINASE_DOW; 1.
PS50011; PROTEIN_KINASE_DOW; 1.
PS50011; PROTEIN_KINASE_DOW; 1.
PS50011; PROTEIN_KINASE_ATP; 1.
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FGR2_HUMAN

2 P21802; P18443;

3 P21802; P18443;

7 01-NOV-1990 (Rel. 16, Created)

7 01-NOV-1990 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (FC

DE (KERATINOCYTE GROWTH FACTOR RECEPTOR).

GN FGFR2 OR BEK OR BFR-1 OR KSAM-1.

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Houssaint E., Blanquet P.R., Champion-Arnaud
Torriglia A., Courtois Y., Breathnach R.;
Torriglia A., Courtois Y., Breathnach R.;
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Dionne C.A., Crumley G.R., Bellot F., Kaplow J.M., Sea Ruta M., Burgess W.H., Jaye M., Schlessinger J.;
"Cloning and expression of two distinct high-affinity cross-reacting with acidic and basic fibroblast growth EMBO J. 9:2685-2692(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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MEDLINE-95235551; PubMed=7719333;

Lajeunie E., Wei M.H., Bonaventure Renier D.;

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Rutland P., Malcolm S.;
Reardon W., Malcolm S.;
Mutations in the third immunoglobulin doma
factor receptor-2 gene in Crouzon syndrome.
... Mol. Genet. 4:1077-1082(1995).
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Malcolm
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Hattori Y., Odagiri H., Nakatani H., Miyagawa K.,
Sakamoto H., Katoh O., Yoshida T., Sugimura T., T
Sakamoto H., Katoh O., Yoshida T., Sugimura T., T
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heparin-binding growth factor receptor genes.";
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Hockley A.D., Hayward R.D., David D.J.
Malcolm S., Winter R.M., Reardon W.;
"Apert syndrome results from localized
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Reardon W., Winter
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"K-sam gene encodes secreted tyrosine kinase.";
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Winter R.M., Rutland P., Pi
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35562; PubMed=7719344;
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factor receptor 2 (FGFR2) gene in Chinese patients with Aper
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J. Craniofac. Surg. 9:207-209(1998).
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SEQUENCE FROM N.A. (LONG FORM).
TISSUE=Brain, and Liver;
TISSUE=Brain, and Liver;
MADDLINE=92228773; pubmed=1373495;
MANSUKHANI A., Dell'Era P., Moscatelli D., Korn
Hanafusa H., Basilico C.;
"Characterization of the murine BEK fibroblast
"Characterization by three members of the FG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601
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DISEASE: DEFECTS IN FGFR2 ARE A CAUSE OF JACKSON-WEISS SYNDROME (JWS) CHARACTERIZED BY CRANIOFACIAL ABNORMALITIES AND ABNORMALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DISEASE: DEFECTS IN FOURZ ARE A CAUSE OF CROUN SYNDROME (CS),
ALSO CALLED CRANIOFACIAL DYSOSTOSIS TYPE I (CFD1). CHARACTERIZED
BY CRANIOSYNOSTOSIS (PREMATURE FUSION OF THE SKULL SUTURES),
HYPERTELORISM, EXOPHTHALMOS AND EXTERNAL STRABISMUS, PARROT-BEAKED
NOSE, SHORT UPPER LIP, HYPOPLASTIC MAXILLA, AND A RELATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFGQVVMAEAVGIDKDKPKEAVTVA-VKMLKDDATEKDLSDLVSEMEMMKMIGKHKNIIN
                                                                                                                                                                                                                                                                                                                                           HAVPSQRPTFKQLVEDLDRILTLTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYYKKTTNGRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEHFWATLIRVPGIPGEISRSAODVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRTNISKEAPPHNIQIFVGSAYFV-----LSQAFVKYIFNNSIVQDFFAWSKDTYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLGACTQDGPL---YVIVEYASKGNLREYLRARRPPGME----YSYDINRVPEEQMTF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L---CGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDLVSCTYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGLARDINNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9693549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1:S18-S19(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.3%;
                                                                                                                                                                                                Last sequence update)
Last annotation update)
TOR RECEPTOR 2 PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                              -AAELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQQRD-W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                             765
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                                           Kornbluth S.,
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    st growth f:
FGF family
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Murinae; Mus
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                  (FGF)
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EMBL; M86441; AAA37286.1; EMBL; M63503; AAA39377.1; EMBL; M63503; AAA37285.1; PIR; A31378; TVMSEK, PIR; A31429; A38429; A38429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requirement Proc. Natl. [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kornbluth S., Paulson K.E., Hanafusa H.;

"Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA libraries.";

MOI. Cell. Biol. 8:5541-5544 (1988).

-!- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACEDISCENSES A HIGHER AFFINITY FOR ACIDIC THAN FOR BASIC FGF'S.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN (A LONG AND A SHORT FORM) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME
                    MOD_RES
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Buropean Bioinformation was long use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (SHORT FORM).
MEDLINE=91095977; PubMed=1846048;
Miki T., Fleming T.P., Bottaro D.P.,
                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; pxinase; 1.
PRINTS; PR00109; TYRKINASE.
PROSITE; PS00107; PROTEIN_KINASE_TYR;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS50011; PROTEIN_KINASE_TYR;
RECEPTOR: 01ycoprotein; Tyrosine-prote
Transferase; Phosphorylation; Transmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89219016; PubMed=2468999;
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DOMAIN
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transforming autocrine loop.";
                                                                                                                                            BINDING
                                                                                                                                                                    NP_BIND
                                                                                                                                                                                    DOMAIN
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Acad. Sci. |
AAA37286.1; -.
AAA39377.1; -.
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                                                                                                                                                                                                                                                                                                                                                                             domain;
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U.S.A. 89:3305-3309(1992).
                                                                                                                                                                                                                                                                                                                                                                             Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                 IN_KINASE_ATP; 1.
IN_KINASE_TYR; 1.
IN_KINASE_DOM; 1.
Tyrosine-protein kinase; ATP-binding;
                                                                                                                                                              FIBROBLAST GROWTH FACTOR RECEPTOR 2
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE DOMAIN.
                                                                POTENTIAL.
                                            POTENTIAL
                                                                                                        PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
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                                                                                                                                              SIMILARITY).
    (GLCNAC.
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CARBOHYD
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Chloroplast.
Eukaryota; Viridiplantae; Em
Eukaryota; Coniferales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               _PINTH __PINTH STANDARD; PRT; 20 YCF2_PINTH STANDARD; PRT; 20 P41653; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence up O1-OCT-2000 (Rel. 40, Last annotation HYPOTHETICAL 244.6 KDA PROTEIN (ORF 20 PROTEIN CORF 20 PAGE 15 PAGE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
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                                                                    "Loss of all ndh genes as determined by sequencing the entire chloroplast genome of the black pine Pinus thunbergii."; Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
-!- FUNCTION: NOT YET KNOWN.
-!- SIMILARITY: BELONGS THE YCF2 FAMILY.
                          This
                                                                                                                                                                                                                       SEQUENCE FROM W....
MEDLINE=95024047; PubMed=7937893;
T-1-204 T Tsudzuki J., Ito S.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Pinus thunbergii (Green pine) (Japanese black pine).
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     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------AAELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQQRD-W
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E -> G (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
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AMLTVALP -> HSGINSSNAEVLALFNVTEMDAGEYICKVS
NVIGOANQSAWLTVLPROQD (IN SHORT ISOFORM).
S -> V (IN REF. 2).
S -> P (IN REF. 2).
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01-MAR-1989 (Rel. 1
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15-DEC-1998 (Rel. 3
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. 10, Created)
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KDA PROTEIN (ORF 2280).

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Query Match
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Chloroplast; Hypothetical protein.
SEQUENCE 2054 AA; 244604 MW; (
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                                                                                                                                                                                                                                                                                                                        864 QTFVLIYDLYRSFNLLTRLNP---FVREKRYLSSIEEISTTPLTKEQI-----
                                                                                                                                                                                                                                                                                                                                                       KVFILFLTLW-LLSLLKLLNVRRLFPQKDIYLVEY-SLSTSPFVRNRYTHVKDEVRYEVN
                                                            LSEI-LLHGSNPFVSILQNIK-HNILLKR-NILWELSHPLWEPIQCKLRTNLIN-----
                                                                                             VSELKKLNGAN----MLETVKPPNSKLERFTYHHELRRVPYEYVKLPIRTNISKEAPPHN
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KFFFPSNNFKDFFPYCKD
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Pred. No. 23;
50; Mismatches
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Chloroplast.
Eukaryota; Viridiplantae; Embryophyta;
Eukaryota; viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core eu
Solanales; Solanaceae; Nicotiana.
              Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashid Matsubayashi T., Zaita N., Chunwongse J., Obokata J., Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.Y. Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa Tohdoh N., Shimada H., Sugiura M.;
"The complete nucleotide sequence of the tobacco chloro its gene organization and expression.";
                                                                                                                                                                                                                                                 Sugiura M
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. BRIGHT YELLOW
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                                                                                                                                                                                 COMPLETE GENOME
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J. 5:2043-2049(1986).
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eudicots; Asteridae; euasterids
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Matches 88
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                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BACITRACIN SYNTHETASE 2 (BA2) [INCLUDES: ATP-DEPENDENT LYSINE ADENYLASE (LYSA) (LYSINE ACTIVASE); ATP-DEPENDENT D-ORNITHINE ADENYLASE (D-ORNA) (D-ORNITHINE ACTIVASE); ORNITHINE RACEMASE (EC_5.1.1.12)].
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Pfam; PF00004; AAA; 1.
Chloroplast; Hypothetical protein.
SEQUENCE 2280 AA; 266812 MW; F
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EMBL; Z00044; CAA77438.1;
PIR; A05204; A05204.
PIR; A05205.
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Sugiura M.;
Submitted (FEB-1998) to the EMBL/GenBanl-
-!- FUNCTION: NOT YET KNOWN.
-!- SIMILARITY: BELONGS THE YCF2 FAMILY
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Pred. No. 26;
67; Mismatches
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Query Match Best Local S Matches 85

Similarity

4 19 . 29 71;

Score 100.5; Pred. No. 37; 71; Mismatches

DΒ

Length

2607; 145;

Gaps

25

Conservative

BINDING

SEQUENCE

AA.

MW;

2094

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REPEAT
REPEAT
DOMAIN
DOMAIN
                                                                                                                                                                                                  PROSITE: PS00012; PHOSPHOPANTETHEINE: 1.
PROSITE: PS0045; AMP BINDING: 2.
PROSITE: PS50075; ACP_DOMAIN: 2.
Ligase: Isomerase: Antibiotic biosynthesis:
Multifunctional enzyme; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INITIATION MODILE), AND EPIMERIZATION (OPTIONAL), AND N
METHYLATION (OPTIONAL), AND N
MISCELLANEOUS: BACITRACIN IS A MIXTURE OF AT LEAST TEN CYCLIC
DODECAPEPTIDES, THAT DIFFER BY ONE OR TWO AMINO ACIDS. THE MOST
ABUNDANT IS BACITRACIN A, A BRANCHED CYCLIC DODECAPEPTIDE. IT
CONTAINS AN N-TERMINAL LINEAR PENTAPEPTIDE MOIETY (ILE-CYS-LEU-D-
GLU-LLE) WITH AN ISOLEUCINE-CYSTEINE THIAZOLLNE CONDENATION
PRODUCT AND A C-TERMINAL HEPTAPEPTIDE RING (LYS-D-ORN-ILE-D-PHE-
HIS-D-ASP-ASN), IN WHICH THE FREE ALPHA-CARBOXY GROUP OF THE C-
TERMINAL ASN IS BOUND TO THE EPSILON-AMINO GROUP OF TYSINE. IT
CONTAINS FOUR AMINO ACIDS IN THE D-CONFIGURATION (GLU-4, ORN-7, PHE-9, AND ASP-11).

-I- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus licheniformis.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions the December 19 of the Property of the P
                                                                                                                                                                                                                                                                                                                          PRINTS; PR00154; PROSITE; PS00012;
                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00501; AMP-binding; Pfam; PF00668; DUF4; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetases.
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"The bacitracin biosynthesis operon of Bacillus licheniformis
10716: molecular characterization of three multi-modular pept;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-ATCC 10716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTIBIOTIC BACITRACIN.
SUBUNIT: LARGE MULTIENZYME COMPLEX OF BA1, BA2 AND BA3.
DOMAIN: CONSISTS OF TWO MODULES WITH A C-TERMINAL EPIMERIZATION
DOMAIN: EACH MODULE INCORPORATES ONE AMINO ACID INTO THE PEPFIDE
PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FO
SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION (NOT FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           m. Biol. 4:927-937(1997).
FUNCTION: ACTIVATES TWO AMINO ACIDS AND INCORPORATE A DEFORM ITS SECOND ACTIVE SITE INTO BACTITRACIN.
CAPALYTIC ACTIVITY: L-ORNITHINE - D-ORNITHINE.
COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETHEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: NON-RIBOSOMAL BIOSYNTHESIS OF THE CYCLIC PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                            AMPBINDING.
                                                                                                                                                                                   0607
ACYL CARRIER (ACP).
ACYL CARRIER (ACP).
PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
MW; FF654FAC5B8BBA6F CRC64;
                                                                                                                                             DOMAIN 1 (LYSINE-ACTIVATING).
DOMAIN 2 (D-ORNITHINE-ACTIVATING).
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                                                                                                                                                                                                                                     Phosphopantetheine;
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01-FEB-1991 (Rel. 1
01-FEB-1991 (Rel. 1
01-FEB-1991 (Rel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paoletti
"The comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-91021027; PubMed-2219722;
Goebel S.J. Johnson G.P., Perkus
Paoletti E.;
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      Goebel S.J., Johnson G.P., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                          COMPLETE GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete DNA sequence of Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccinia virus (strain Viruses, dsDNA viruses, Orthopoxvirus.
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                                                    EMBL; M35027; AAA48053.1;
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Best Local S
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01-NOV-1990 (
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                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
              Pfam; PF00047; ig; 3.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
TYROSINE KINASE RECEPTOR CEK3 PRECURSOR (EC
                                                                                               EMBL; M35196; AAA48665.1;
PIR; B35963; B35963.
HSSP; P11362; 1FGI.
                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 87:5812-5816(1990)
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEI
-!- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH
                                                                                                                                                                                                                                                                                                                                            Pasquale E.B.;
"A distinctive family of embryonic
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Marchosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken)
                                                    InterPro; IPR000719; -.
InterPro; IPR001245; -.
InterPro; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                 receptors.";
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  PROSITE;
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nes 75; Conserv
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PROSITE; PS50011; PROTEIN_KINASE_DOW;
Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                             693
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     743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 CFSNIFIASKL------EAVEYAHISRLQADL--NCLSDL-----LKSSIQWKYVIN 225
ITLPSEK-LF-----MDRNLTTTS 453
                                                                                                          VLMWEIFTLGGSPYPGIPVEELFKLLKEGH----RMDKPAN-----CTNE-LYMMMRDCW 742
                                                                                                                                                                                                                   DYYKKTTNGRLP----
                                                                                                                                                                                                                                                                                                                                                                        IRTNISKEAPPHNIQIFVGSAYFV------LSQAFVKYIFNNSIVQDFFAWSKDTYSP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L---CGQDFPLKSNFELVSELKKLNGANMLETVKPPNSKLERFTYHHELRRVPYEYVKLP
                                                                                                                                                                                                                                                                  DEHFWATLIRVPGIPGEISRSAQDVSDLQSKTRLVKWNYYEGFFYPSCTGSHLRSVCIYG
                                                                                                                                                                                                                                                                                                                        -----KDLYSCTYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGLARDINNI
                                                                                                                                                                                                                                                                                                                                                                                                                                LLGACTQDGPL---YVIVEYASKGNLREYLRARRPPGME----YSFDINRVPEEQMTF-
                                                                                                                                                          ------AAELRWLIKDGHWFANKFDSKVDPILIKCLAEKLEEQQRD-W 435
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ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

POTENTIAL.

POTENTIAL.

POTENTIAL.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE DOMAIN.

IG-LIKE DOMAIN.

IG-LIKE DOMAIN.

ASP/GLU-RICH (HIGHLY ACIDIC).

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).
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TYROSINE KINASE RECEPTOR CEK3.
EXTRACELLULAR (POTENTIAL).
  767
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Search completed: August Job time: 298 sec

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2001, 14:50:18

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                       N_Geneseq_0601:*

1: /SIDSB/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDSB/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDSB/gcgdata/geneseq/geneseqn/NA1983.DAT:*
4: /SIDSB/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDSB/gcgdata/geneseq/geneseqn/NA1983.DAT:*
6: /SIDSB/gcgdata/geneseq/geneseqn/NA1985.DAT:*
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15: /SIDSB/gcgdata/geneseq/geneseqn/NA1993.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Result		% Query				
No.	Score	Match	Match Length DB	B	ID	Description
<b>ji</b>	1362	100.0	1362	22	AAS00045	Human DNA encoding
N	191.8	14.1	1221	21	AAA96575	Core 2 beta-1,6-N-
ω	191.8	14.1	1317	21	AAA96569	DNA encoding a cor
4	191.8	14.1	2108	21	AAA96570	A core 2 beta-1,6-
υı	191.8	14.1	2128	22	AAC62134	Nucleotide sequenc
o	191.8	14.1	2229	21	AAC99109	Human pancreatic c
7	191.8	14.1	2319	21	AAA48623	Human C2/4GnT cDNA
œ	185.2	13.6	1807	16	AAQ89201	I-branching enzyme
9	185.2	13.6	1807	17	AAT16201	Beta-1,6-N-acetylq
10	185.2	13.6	1807	19	AAV30006	Full length cDNA s
11	185.2	13.6	1807	19	AAV16000	Human beta-1,6-N-a

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n gene	lung tumo	C-termina	Human secreted pro	E. coli J96 pathog	Oligonucleotide D1	Oligonucleotide D1	Streptococcus pneu	Human secreted pro	n secre	ne bet	n colon	secre	catal	Oligonuclectide D1	nucleotide	ligonucleotide	ligonucleotide	ligonucleotide	igonucleotide	ligonucleotide	igonucleotide	ligonucleotide	ligonucleotide	idonucleotide	ligonucleotide	A encoding a	ng sequence f	n heart core	an core 2GnT D	betic rat hear	OH1 cDNA.	sequence of	Human secreted pro

## ALIGNMENTS

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RESULT AAS00045 Human; C2GnT3; Thymus-related disorder; cancer; tumour; adenoma; UDP-GLONAC: Galbeta1,3GalNAc alpha-R beta1,6GlONAC transferase; sarcoma malignant melanoma; breast cancer; certal cancer; hypoactivity; hyperactivity; atrophy; thymus enlargement; autoimmunity; arthritis; leukaemia; lymphoma; immunosuppression; AIDS; Wiskott-Aldrich syndrome; acquired immunodeficiency syndrome; sepsis; wound healing; infection; d 14-MAY-2001 (first entry) AAS00045 standard; DNA; 1362 Homo sapiens. Human DNA encoding C2GnT3. AAS00045; ВP

sarcoma;

01-MAR-2001. CDS primer\_bind primer\_bind WO200114535-A2 /\*tag= b
/label= "Binding site
1347..1362 /\*tag= a
/product= "C2GnT3"
complement (114..138) Location/Qualifiers
1..1362 'label= "Binding site for for PCR primer TSHC121" PCR primer TSHC100"

24-AUG-2000;

2000WO-DK00469

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The sequence encodes Human UDP-N-acetyl-glucosamine:Galactose-betal, CC 3-N-acetylgalactosamine-alpha-R betal-6 N-acetylglucosaminyltransferase CC (UDP-GLONAC: Galbetal,3GalNAC alpha-R betal,6GlCNAC transferase or CC 273073). C23073 and nucleic acids encoding it are useful in the CC particularly a thymus-related disorder. C23073, nucleic acids encoding it are useful in the CC particularly a thymus-related disorder. C23073, nucleic acids encoding it and antibodies against it may also be used for in vitro CC encoding it and antibodies against it may also be used for in vitro CC encoding it and intibodies against it may also be used for in vitro CC exectors, in the prognostic and diagnostic evaluation of conditions CC associated with altered expression or activity of C23073 or conditions CC associated with altered expression or activity of C23073 or conditions CC experision and localising the DNA and protein, Disorders such as tumours CC (e.g. malignant melanoma, adenoma and sarcoma) and cancers (e.g. of the breast or cervix), hypoactivity, hyperactivity, atrophy, enlargement of CC breast or cervix), hypoactivity, leukamia, lymphomas, immunosuppression, CC acquired immunodeficiency syndrome (AIDS), Wiskott-Aldrich syndrome, CC sepsis, wound healing, acute and chronic infection, cell-mediated or chumour immunity, or THJ/TH2 imbalance, may be treated using these protein CC or nucleic acid. The antibodies may be used to screen potential CC therapeutic compounds to determine their effects on a conditions such as thymps-related disorder or cancer, to determine the level of C26073 or to detect and quantify polypeptides in a sample to determine their role in a particular cellular events or pathological states and to diagnose and CC creat such pathological states and to diagnose and
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Best Local Similarity 100.0%;
Matches 1362; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New C2GnT3 polypeptides and nucleic acids encoding the polypeptides useful for treating conditions mediated by a C2GnT3 polypeptide, e.g., thymus-related disorders, cancers, tumours, immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1362 BP;
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P-PSDB; AAU00037.
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CLAUSEN H.
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RESULT AAA96575

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1200	agttgtactggatctcaccttcgaagcgtgtgtatttatggagctgcagaattaaggtg	4	Qy
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1020	gttcaagacttttttgcctggtctaaagacacatactctcctgatgagcacttttgggct	961	Qy
960	gcagtgcttattttgttttaagtcaagcatttgttaaatatattttcaacaactccatc	90:	Дb
960	ggcagtgcttattttgtttttaagtcaagcatttgtttaaatatattttcaacaactccatc	901	Qy
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780	toagagttgaaaaaactcaatggagcaaatatgttggagacggtgaaacccccaaacagt	721	Дb
780	tcagagttgaaaaaactcaatggagcaaatatgttggagacggtgaaaccccccaaacagt	721	Qy
720	aaatatgttatcaacttgtgtgggcaagattttcccctgaagtcaaattttgaattggtg	661	Дb
720	aaatatgttatcaacttgtgtgggcaagattttcccctgaagtcaaattttgaattggt	661	Qy
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660	tecagaetecaggetgatttaaattgettgteggaeettetgaagtetteaatecagt	601	Qy .
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540	tgcatccattatgatcgtaaggcacctgataccttcaaagttgccatgaacaatttagc	481	Db
540	tgcatccattatgatcgtaaggcacctgataccttcaaagttgccatgaacaatttag	481	Qy
480	l aaagatgcaattatggttgaaaggcttatccatgctatatacaaccagcacaatatttac	421	Дb
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360	l gatgatgttgtggcaatgaccagtgattgtgacatttatcagactctaagaggttatgct	301	дд

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                                                                                                                                                Query Match
Best Local Similarity
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a-1,6-N-acetylglycosaminyltransferase (core2b GlcNac-T) polypeptide
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ttgaaaggcttatccatgctatatacaaccagcacaatatttactgcatccattatgatc
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AAA96569 standard; DNA; 1317 ВP

08-FEB-2001 entry)

DNA encoding ۵ core 2 beta-1,6-N-acetylglycosaminyltransferase.

Core 2 beta-1,6-N-acetylglycosaminyltransferase; core2b GloNAc-T; cancer; cardiovascular disorder; inflammatory disorder; asthma; rheumatoid arthritis; inflammatory bowel disease; arteriosclerosis; septic shock; adult respiratory distress syndrome; ARDS; cancer;

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beta-1,6-N-acetylglycosaminyltransferase'
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Pred. No. 4.3e
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                              platelet-mediated pathology; atherscierosis; g
clotting; ascites; cholelithiaseis; cirrhosis;
diverticulitis; ulcerative colitis; ss.
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                                                                                                        Core 2 beta-1,6-N-acetylglycosaminyltransferase; core2b
cancer; cardiovascular disorder; inflammatory disorder;
                                                                                                                                                                                       08-FEB-2001
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                                                                        septic shock; adult respiratory distress syndrome; ARDS; cancer;
                                                                                          rheumatoid arthritis; inflammatory bowel disease; arteriosclerosis;
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                                               gastrointestinal disorder;
s; Crohn's disease;
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Best Local Similarity
Matches 517; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a partial human core 2 beta-1,6-N-acetylglycosaminyltransferase (core2b GlcNac-T) polypeptide. The polypeptide can be used to treat diseases and disorders, such as cancer, cardiovascular disorders and inflammatory disorders including asthma, rheumatoid arthritis, inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecules of core 2 beta-1,6-N-acetylglycosaminyltransferase useful for providing a compositions for treatment of disorders mediated by the enzyme including cancer, cardiovascular and inflammatory disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immuno-histochemical analysis, to detect the novel polypeptide localize it to particular cells and tissues and to specific subscations and to quantitate the level of expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New C2GnT-M polypeptides having core 2, core 4 and I branching beta-1-6-N-acetylglucosaminyltransferase activities for preparing reagents useful for diagnosing, preventing or treating inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2128
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AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be u
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                       The present sequence encodes human UDP-N-acetylglucosamine:
N-acetylgalactosamine beta-1,6-N-acetylglucosaminyltransferase
(C2/4GnT). The protein is the third member of the family of O-glycan
beta-1,6-N-acetylglucosaminyltransferases. It adds core 2 or core 4
                                                                                                                                                                                           New nucleic acid molecule encoding UDP-N-acetylglucosamine useful probe for the detection of specified glucoseaminyltransferase from other species and related organisms \cdot
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Query Match Best Local S Matches 502

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                    reverse-transcribed and inserted into expression vector pcDNAL Plasmid DNA was used to transfect CHO-Py-leu cells. Transfected cells were screened using human anti-I antigen antibodies and god anti-human IgM. Plasmid DNA was analyzed to obtain DNA (given in AAQ89201) encoding I-branching enzyme (AAR71932).
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Sequence 1807 BP; 511 A; 401 C;
                                                                                 Poly-A RNA isolated from human PA-1 teratocarcinoma cells
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P-PSDB; AAR92474.
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δÃ A cDNA insert (AAT16201) in pcDNAI-IGhT codes for human beta-1,6-N-acetylglucosaminyltransferase, I-branching enzyme (IGhT) (AAR92474), an enzyme that converts blood group i antigen to I antigen. The cDNA was isolated from a cDNA library pred. from human PA-1 teratocarcinoma cells in vector pcDNAI following transfection into CHO-Py-leu cells and screening with human anti-I antibodies. The cDNA can be used to regulate the expression of human IGhT or to modify its biological function, to produce soluble or membrane-bound forms of IGhT in host cells, to breed transgenic animals, and to design anticenses. Human beta-1,6-N-acetyl:glucosaminyl transferase, used to develop prods. for the study, detection pathological conditions involving the enzyme. Beta-1,6-N-acetylglucosaminyltransferase, I-branching enzyme; IGnT; glycosyltransferase; blood group; I antigen; polylactosaminoglycan; Beta-1,6-N-acetylglucosaminyltransferase, design antisense oligonucleotides Example 4; Column 29-32; 29pp; English 707 327 ttgtgacatttatcagactctaagaggttatgctcaaaaggttgtctcaaaggaggagaa 386 tatccatgctatatacaaccagcaccaatatttactgcatccattatgatcgtaaggcacc aagetteecaatageetattetttggttgteeaeagatgeaattatggttgaaagget ttgcaaggaatacttgacccagagccactacatcacagcccctttatctaaggaagaagc 526 ttccaagatggaacccgttgtctatggagggatctccaggctccaggctgacctgaactg ttccaaattagaggctgtggaatatgcccacatttccagactccaggctgatttaaattg aactgaatttaaagatgcggtagagcaactattaagctgcttccccaaacgcttttctggc tgataccttcaaagttgccatgaacaatttagctaagtgcttctccaatattttcattgc tgactttcccttggcatatataatggtcatccatcatcactttgacacctttgcaaggct cttcagggctatttacatgccccaaaatatctactgtgttcatgtggatgaaaaagcaac 93US-0118906 93US-0118906 Location/Qualifiers 255..1457 511 A; 13.6%; 52.1%; RES 3 401 C; 0; Score 185.2; DB 1 Pred. No. 3.5e-42; 0; Mismatches 438 398 G; 497 T; I-branching DB 17; 438; 0 other I-branching enzyme and treatment of Length 1807; 24; Gaps 626 566 506 586 446 766 706 646

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                                                                                                                              Human; beta-1,6-N-acetylglucosaminyltransferase; I-branching enzyme; IGnT; core 2-beta-1,1-N-acetylglucosaminyltransferase; C2GnT; treatment; disorder; under expression; type-II hypersensitivity reaction; neonatal haemolytic disease; autoimmune haemolytic anaemia;
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            07-JUN-1995;
                                                                US5766910-A
                                                                                         Homo sapiens
                                                                                                                   thrombocytopenia;
                                                                                                                                                                                                 Full length cDNA sequence of human
                                                                                                                                                                                                                            11-AUG-1998
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Similarity

13.6%;

Score 185.2; DB 19; Pred. No. 3.5e-42; Mismatches

Length

1807 24;

Gaps

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Conservative

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beta-1,6-N-acetylglucosaminyltransferase, the I-branching enzyme (IGnT). The protein sequence has a type II transmembrane topology that consists of a short amino terminal cytoplasmic sequence, a signal-anchor sequence followed by a short stem region and a large carboxyl terminal catalytic domain. The protein shows some homology to core 2-beta-1, N-acetylglucosaminyltransferase (2GnT). The nucleic acid sequence is used for producing IGnT polypeptides, which can be used to treat disorders arising from under expression of IGnT, e.g. increased susceptibility to type-II hypersensitivity reactions such as neonatal haemolytic disease, autoimmune haemolytic anaemia and thrombocytopenia.
                                                                                                                                                                                                                                                                                                  Claim 2; Columns 29-32; 31pp; English.
                                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences and their complementary sequences - useful for producing fragment of recombinant human I-branching -1,6-N-acety1-glucosaminy1-transferase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-361697/31
P-PSDB; AAW56628.
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Sequence 1807 BP; 511 A; 401 C; 398 G; 497 T; 0 other;
                                                                                                                                                                                                                                      The present sequence encodes human beta-1,6-N-acetylglucosaminyltrans
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antigen binding fragment; antibody; I-branching
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                        Disclosure;
                                                                  beta-1,6-N-acetyl-glucosaminyl-transferase - useful for, imaging IGnT-containing sites in vivo as IGnT is involved the cell adhesion to endothelium
                                                                                                                                                                                                                                                        Bierhuizen MFA,
                                                                                                                                                                                                                                                                                                  (LJOL-) LA
                                                                                                                                       Antibodies to human I-branching
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This cDNA encodes a human beta-1,6-N-acetylglucosaminyltransferase, I r-branching enzyme (IGnT). This nucleic acid encodes both the soluble and membrane-bound IGnT. This nucleic acid encodes both the soluble specifically reactive with IGnT or an active fragment comprising a catalytic domain of IGnT. These anti-IGnT antibodies can be used to detect IGnT or IGnT-expressing cells in biological samples, e.g. to human cDNA expression libraries, to purify IGnT from compositions containing it, or to image IGnT-containing sites in vivo as IGnT is involved in tumour cell adhesion to endothellum and leuxocyte adhesion to inflammatory sites.
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Pred. No. 3.5e-42;
0; Mismatches 438;
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                           δÃ
                                                                                   Query Match 13.4%;
Best Local Similarity 100.0%;
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                        The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 23284; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
                                                                                                                                                                                                                                 Sequence 186
                                                                                                                                                                                                                                                                                         expression and secretion vectors.
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tttaaccctatggctgctctctttgttaaaggcttctaaatgtgagacgactctttccgca 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tag; secreted protein; cDNA isolation;
phromosome mapping; ss.
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                                                                                   score 183; DB; Pred. No. 5.4
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                O-glycan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequence of human core 2 beta 1-6 N-acetylglucosaminyltransferase (C2GnT or core 1-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ61559;
                                                                                                                                                                                                                                                                                                                                            misc_signal
                                                                                                                                                                                                                                                                                                                                                               polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          C2GnT; 1-6 AGT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ61559 standard; cDNA; 2105
                                                                                                                                         New beta 1-6 N-acetyl:glucosaminyl transferase and acceptor used for the study of the effect of variant O-glycan(s) on cell-cell interactions, partic. in cancers
                                                                                                                                                                                                            Bierhuizen MFA,
                                                                                                                                                                                                                                                01-OCT-1992;
                                                                                                                                                                                                                                                                                     06-APR-1994
                                                                                                      C2GnT, or an active fragment thereof,
                                                                                                                        Disclosure; Page 20-22; 34pp; English
                                                                                                                                                                                                                                                                    29-SEP-1993;
                                                                                                                                                                                                                                                                                                       EP590747-A.
                                                                                                                                                                                P-PSDB; AAR51386
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/label= signal/membrane-anchoring domain
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220. 1504
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                                                                                                                                                                                                                                                                                                                                                                                                                                           2 beta 1-6 n-acetylglucosaminyltransferase;
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critical branches in O-glycans. cDNAs encoding various glycosyltransferases can be isolated by transfert expression of in recipient cells, e.g. COS-1. COS-1 cells were transfected with a cDNA library, pcDSR alpha-2F1, constructed from poly(A)+ of activated T lymphocytes which express the CZGNT. Transfected cells were selected using MAb T305, which identifies a hexasaccharide on leukosialin. Leukosialin CD43 is an acceptor molecule for CZGNT activity. A plasmid, pcDSR alpha-Leu, which directed expression of the T305 antigen was identified. The CDNA insert was isolated and sequenced. The cDNA encoded the acceptor molecule leukosialin CD43.

The

CDNA

RNA

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Query Match
Best Local
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  1242 taaggtggaccctatcttgattaaatgcttggcaga 1277
                                            1371 agctggtgacttgaactggatgctgcgcaaacaccacttgtttgccaataagtttgacgt 1430
                                                                                                                                    1311 caagggtgctccctacccgccctgcgatggagtccatgtgcgctcagtgtgcattttcgg
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les 517; Conser
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                                                                          agctgcagaattaaggtggcttatcaaagatggacattggtttgctaataaattttgattc 1241
                                                                                                                                                                                                                                atctgacatgcaagcagttgccaggtttgtcaagtggcagtactttgagggtgatgtttc 1310
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                                                                                                                               This invention describes a method for screening for a substance that CC may be used to prevent or treat cardiomyopathy associated with diabetes. CC and hyperglycaemia. This method involves reacting core 2 GlCNAc-TC (UDP-GlCNAc:Galbetal-3GalNAc-alphar beta-1,6-N-acetylglucosaminyl-CC transferase) with an acceptor substrate and a sugar nucleotide donor in CC transferase) with an acceptor substrate and a sugar nucleotide donor in CC product, and comparing the amount of reaction product with the amount of product, and comparing the amount of reaction product with the amount CC product, and comparing the amount of reaction product with the amount CC reaction product in the presence of the test substance indicate that the CC substance inhibits core 2 GlCNAc-T. The invention also describes (1) CC methods for preventing or treating cardiomyopathy associated with CC diabetes and hyperglycaemia, and (2) transgenic nonhuman animal whose CC germ cells and somatic cells all contain a DNA construct introduced into the animal or an ancestor of the animal at an embryonic stage, where construct animal to develop cardiomyopathy associated with diabetes mellitus and hyperglycaemia. This sequence encodes the rat CC child bettes mellitus and hyperglycaemia. This sequence encodes the rat CC child protein which is used to describe the method of the invention.
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Best Local Similarity
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    1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preventing or treating cardiomyopathy associated with diabetes mellitus and hyperglycemia, comprises administering a substance that inhibits core 2 N-acetylglucosamine-T activity -
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Search completed: August 3, 2001, 01:06:11 Job time: 3253 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_estro23:\*
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em\_estro21:\*
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Result No.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 821)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1995)
Contact: Robert Strausberg, Ph.D.
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BE866192 601445191
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AW233232 fj29g12 y
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BE863271 UI-M-BHO-BF416867 UI-R-CNO-BF416867 UI-R-CNO-BF416867 MRZ-ST013
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                                                                        AATCTCACTACCACATCATGA 441
                                                                                    aatctcactaccacatcatga 1362
                                                                                                                                CGAAGCGTGTGTATTTATGGAGCTGCAGAATTAAGGTGGCTTATCAAAGATGGACATTGG
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                                                                                                                   AQ005888 410 bp DNA GSS 27-JUN-1998 CIT-HSP-2288B17.TF CIT-HSP Homo sapiens genomic clone 2288B17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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/db_xref="taxon:9606"
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Pred. No. 3.2e
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174.2 170.8 163.2 157.6

REFERENCE AUTHORS TITLE

COMMENT

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ACCESSION VERSION DEFINITION

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RESULT BG434801 LOCUS

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ataaatttgattotaaggtggaccotatottgattaaatgottggcagaa 1278
                                                                                                               agtggaattactatgaaggctttttctatcccagttgtactggatctcaccttcgaagcg
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                                                         tgtgtatttatggagctgcagaattaaggtggcttatcaaagatggacattggtttgcta
                                                                                                 AGTGGAATTACTATGAAGGCTTTTTCTATCCCAGTTGTACTGGATCTCACCTTCGAAGCG
                                          TGTGTATTTATGGAGCTGCAGAATTAAGGTGGCTTATCAAAGATGGACATTGGTTTGCTA
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AQ005888
AQ005888.1
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Use of a random BAC End Sequence Database
Building (1998)
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1 (bases 1 to 410)
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are available from Research Genetics (info@resgen.com). BA end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html seg primer: M13·21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Other_GSSs: CIT-HSP-2288B17.TR
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Golden,K., Berry,K., Granger,D., Suh,E., Wible,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mdadams@tigr.org
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Medical Center Dr., Rockville,
301 838 0200
301 838 0208
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/note="Vector: pBeloBAC11; Site_1:
HindIII"
87 c 81 g 107 t
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/db_xref="GDB:7149764"
/db_xref="taxon:9606"
/clone="2288B17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
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99.8%;
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C., Shizuya,H.,
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ATAAATTTGATTCTAAGGTGGACCCTATCTTGATTAAATGCTTGGCAGAA
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                      totgatotgoagagtaagaotogoottgtoaagtggaattaotatgaaggotttttotat 1137
                                                                                 GTTACCTTGATTCGGGTTCCAGAAATACCTGGGGAGATTTCCAGATCAGCCCAGGATGTG
                                                                                                     gctaccttgattcgggttccaggaatacctggggagatttccagatcagcccaggatgtg 1077
TCTGATCTGCAGAGTAAGACTCGCCTTGTCAAGTGGAATTACTATGAAGGCTTTTTCTAT
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427; Conservative
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HS_2175_B1_A12_T7 CIT Approved Human Genomic Sperm Library D
sapiens genomic clone Plate=2175 Co1=23 Row=B, DNA sequence.
A0900348
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 612)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Meller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2175 row: B column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 612 Location/Qualifiers
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Class: BAC ends
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Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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/db_xref="taxon:9606"
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/sex="male"
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Pred. No. 3.1e
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Utah Genome Cer
University of Utah
Rm. 308, Biomedical Polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0422 row: E column: 09
Seg primer: CGTTGTAAAACGACGGCCAGT
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Fax: 801 585 7177
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quality sequence stop: 590
Location/Qualifiers
                                    was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TA DNA polymerase and TA polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                   /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC1M0422E09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene)
                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Rodentia;
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REFERENCE AUTHORS VERSION KEYWORDS COMMENT SOURCE ACCESSION DEFINITION LOCUS RESULT 5 AQ091453/c JOURNAL MEDLINE TITLE ORGANISM AQ091453 292 bp DNA GSS 26-AUG-199 HS.3016\_B1\_A10\_T7 CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=3016 Col=19 Row=B, DNA sequence. AQ091453 AQ091453.1 GI:3460364 High Throughput Sequencing University of Washington Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center Sequence-tagged connectors: A sequence scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 292)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Walairas,G.G., Wallace, Terlong,J., Young,J., Zhao,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Hood (17), approach to 9739-9744 (1999) mapping Library D Homo Holzman,T., Adams,M.D.

nigroviridis

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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3016 row: B column: 19
Class: BAC ends
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                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 908)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
2 (bases 1 to 908)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetie Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide ana
                                                                                                                                                                                                                  GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
                                                                                                                                                                                                                                               AL188089.1 GI:7826193
GSS; genome survey seq
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E-Coli DH10B"
a 62 c 57 g 70 t 2 other;
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/db_xref="taxon:9606"
/clone="Plate=3016 Col=19
/clone_lib="CIT Approved F
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Pred. No. 3.2e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaggagaaaagcttcccaatagcctattctttggttgtccacaaagatgcaattatggtt 438
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GTGGCCAAAGCCCCGCCCCCCMGCCGGCATCCAGGTCTTCATCGGCAGCGCCTATTTCGWC
                               atotocaaggaagcaccccccataacattcagatatttgttggcagtgcttattttgtt
                                                                                                                             taccatcatgaacttagacgggtgccttatgaatatgtgaagctaccaataaggacaaac 858
                                                                                                                                                                                               AACGGCAGCAACATGCTGGAGAGCAGCCGGCCCAGCGAGCTGAAGAAGCAGCGCTTCCTC
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                                                                                                                                                                                                                                                                                               TGCGGCCAGGACTTTCCCCTCCGGACCAACTACGAGCTGGTGAGGGAGCTGAAGGAGCTG
                                                                                                                                                                                                                                                                                                                    tgtgggcaagattttcccctgaagtcaaattttgaattggtgtcagagttgaaaaactc
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                                                                                                  TTCCAGCACCAGCTGAAGAGCGCGCCCTACGAGTACCGGCGCATTCCTGTCAAAACCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome. For more information, please thttp://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
/clone="251C11"
/clone_11b="G"
/note="Genoscope sequence ID : COA
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Pred. No. 2.2e-57;
7; Mismatches 347;
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                                                                                                                                                                            actcatgttaaggatgaagtcaggtatgaagttaactgttcgggtatctatgaacaggag 240
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                                                                                                   cctttggaaattggaaagagtctggaaataagaagaagggacatcattgacttggaggat 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTCAGCTGACACCTACTCGCCGGACGAGC
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                                                                                                                                                       AATGGTGTTCAGGCCTACAACACGTACAATGTTAACTGTCCCGCGATATACGAAATGGAC 569
GAAAGCCTGACCAAACTGACCTCTGACTGCAGGATGTTTGTCAGGGCCAGAGGTTACGAC
                                 gatgatgttgtggcaatgaccagtgattgtgacatttatcagactctaagaggttatgct 360
                                                                          CCGATGGAGGTGGGGAAGTCCTTGATCATCCGGAGGAAACCTCTGCCGCCGGAGTCGGAC
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Tetraodon nigroviridis genome survey sequence T3
039H15 of library A from Tetraodon nigroviridis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large-scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a lock at http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
/clone="039H15"
/clone_lib="A"
/clone_lib="A"
/note="Genoscope sequence ID :: C0AA039CD08A1~end
234 c 261 g 231 t 7 others
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                                                                                                                                                                                                                                Score 221; DB 222;
Pred. No. 9.7e-49;
D; Mismatches 250;
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                                                   Shibat., K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Karada, A., Yamamoto, R., Matsumoto, H., Szakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsundra, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (strain:C57BL/6J) adult male pituitary gland cDNA mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:5330430K10.
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Shibata,K.,
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High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria;
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exploration Research Group, RIKEN Gemomic Sciences Center (3 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, yoj Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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excision from Lambda FIC I. Cloning sites, 5' end: Sall;
BamHI. Host: DH10B.
   Conservative
                                                                                                                                                                                                                                                                                         /protein_id="Bab31918.1"
/db_xref="GI:12860327"
/db_xref="GI:12860327"
/translation="MSIGKVFAVSALSVVIFVVFYHSQLSLPNLYQQLNSSSERTSV
/TICDXGLQMPFFFTTGGTSPHPLERLSCPQYRIQSHYITSPLSEEBAAPPLAYIMVIH
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GFSRLQADLNCMKDLVASKVFWKYVLNTCGQDFPLKTNKEIINHLKRFKGKNITPGVL
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GGCHGKVSRSGATLPVADPRQL"
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/db_xref="MGD:MGI:1912211"
/db_xref="MGD:MGI:1925531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="putative"
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                            13.7%;
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DEFINITION
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                                                                                                                        AUTHORS
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AK008234.1 GI:12842295
CAP trapper.
Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK008234 1862 bp mRNA HTC 08-FEB-2001 Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010013H22, full insert sequence.
                                                                                                                                                                   High-efficiency full-length cDNA cloning methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                   clone:2010013H22.
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; Murinae; Mus
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Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Horl, F.,
Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J.,
Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Okido, T., Owa, C., Saito, H., Saito, R., Sakai, K., Sano, H.,
Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, The Institute of
Submitted (10-JUL-200) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P. Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Kikuchi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y., Matsuura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y., Sakaguencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functional annotation of a Nature 409, 685-690 (2001) 5 (ases 1 to 1862)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5' GAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)

Fax:81-45-503-9216)

Fax:81-45-503-9216)
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Shibata,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adachi, J., Alzawa, K., Akahira, S.,
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/protein_id="BAB25548.1"
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/db_xref="GI:12842296"
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KIENFERLLRAVYTPQNVYCVHMDQKSSEPFKQAVRAIVSCFPNVFIASKLVSVVYXAS
                                                                                                                                                        /dev_stage="adult"
240. .1436
                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                   /tissue_type="small intestine"
/clone_lib="RIKEN full-length
                                                                                                                                                                                                                                                                                         /db_xref="MGD:MGI:1904808"
/db_xref="MGD:MGI:1919327"
                                                                                                                                /note="putative"
                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Fukunishi,Y., Furuno,M.,
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WSRVQADLNCMEDLLQSPVPWKYLLNTCGTDFPIKTNAEMVKALKLLKGQNSMESEVP
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QLIEWYKDTYSPDEHLMATLQRASWMPGSDPLHRKFDMSDMRAIARLTKWYDHEGDIE
NGAPYTSCSGIHQRAVCVYGSGDLHWILQNHHLLANKFDPKVDDNVLQCLEEYLRHKA
IYGTEL"
484 a 463 c 478 g 437 t
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438 ATGACAGCAGACTGTGAGCACTTCAAGACCAAGAGGAAGTTTATACAGGTCCCACTGAGC 497 316 atgaccagtgattgtgacatttatcagactctaagaggttatgctcaaaaagcttgtctca 498 AAGGAAGAGGCCAGCTTCCCCATTGCGTACTCCATGGTGCTGCATGAGAAGATTGAGAAC aacatctccaaggaagcaccccccataacattcagatatttgttggcagtgcttatttt ctcaatggagcaaatatgtttggagacggtgaaacccccaaacagtaaattggaaagattc ttgtgtgggcaagattttcccctgaagtcaaattttgaattggtgtcagagttgaaaaaa gatttaaattgcttgtoggaccttotgaagtottoaatocagtggaaatatgttatcaac GTCTTCATAGCTAGTAAGTTGGTGTCAGTGGTCTATGCTTCCTGGTCCAGGGTGCAGGCT attttcattgcttccaaattagaggctgtggaatatgcccacatttccagactccaggct CAGAAGTCTTCAGAACCCTTTAAGCAGGCAGTCAGGGCCATCGTGTCATGCTTCCCCAAT gttgaaaggcttatccatgctatatacaaccagcacaatatttactgcatccattatgat 495 aaggaggagaaaagcttcccaatagcctattctttggttgtccacaaagatgcaattatg 435 gcctggtctaaagacacatactctcctgatgagcacttttgggctaccttgattcgggtt 1035 gttttaagtcaagcatttgttaaatatattttcaacaactccatcgttcaagactttttt acttaccatcatgaacttagacgggtgccttatgaatatgtgaagctaccaataaggaca TTGAAAGGGCAGAACAGTATGGAGTCAGAGGTACCACCTCCACATAAAAATCCCGGCTGG ACCTGTGGGACAGACTTTCCCATCAAAACCAATGCTGAGATGGTCAAGGCCCTCAAGCTA GACCTAAACTGCATGGAAGACTTGCTTCAGAGCCCCGTGCCATGGAAATACCTCCTGAAC cgtaaggcacctgataccttcaaagttgccatgaacaatttagctaagtgcttctccaat TTCGAAAGGTTGCTGCGAGCTGTGTACACCCCCTCAGAATGTATACTGTGTCCACATGGAT ACGTCTTGCTCAGGAATCCACCAGCGGGCTGTCTGTGTTTATGGGTCAGGGGACCTGCAC cccagttgtactggatctcaccttcgaagcgtgtgtatttatggagctgcagaattaagg 1197 aagactcgccttgtcaagtggaattactatgaaggcttttt----TOGTGGATGCCTGGATCAGATCCCTTGCATCGAAAATTTGACATGTCAGACATGAGAGGCC 1196 ccaggaatacctgg---ggagatttccagatcagcccaggatgtgtctgatctgcagagt 1092 GAGTGGGTAAAAGACACCTATAGTCCCGATGAGCACCTTTGGGCCACCCTCCAGCGTGCC GTGGCTTCTCGAGACTTCATTGAACACGTGTTCAGTAACTCAAAAGCCCGGCAACTGATC AGCAAGAGGAAGACGCCGCCACCTAATAACCTAACCATGTTCACTGGGAATGCCTACATG AAATATCACTATGAGGTGACA----ATTGCGAGACTAACCAAGTGGTACGACCATGAGGGAGACATTGAGAACGGGGCACCTTAC Similarity Conservative 12.8%; 0; Score Pred. Mismatches 174.2; DB 1 No. 4.8e-36; 192; -GACACATTGCACATGACC Length 1862, ----ctat 1137 Gaps 975 915 1076 1016 795 555 1136 956 855 917 857 797 675 615 677 617 1256 ω

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 TGTCTATGGGGKGATCTCCADGCTCCAWGCTGACCTGAACTGCCTGGAAGACCTTGTGCC
                              ggaatatgcccacatttccagactccaggctgatttaaattgcttgtcggaccttctgaa 644
                                                                                       catgaacaatttagctaagtgcttctcccaatattttcattgcttcccaaatttagaggctgt
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1 (bases 1 to 860)

11.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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mRNA sequence.
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/clone="CS0DI072YD06"
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2 (bases 1 to 970)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., E Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, Burin, W. and Weissenbach, J.

Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide anal.

The province of the provided by genome wide anal.
                                                               Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a scale clone-end sequencing project of the Tetraodon nigrovirid genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot
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/organism="Tetraodon nigroviridis"
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/clone="042K19" /clone\_lib="A"

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ALI68380.1 GI:7806437
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Loases 1 to 756)
Roset-Crollius.H., Jaillon,O., Dasilva,C., Bouneau,L.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Queties
Saurin,W. and Weissenbach,J.
Human gene number Pottanian
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrov-genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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MRO-BN0115-020300-001-a03 BN0115
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Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Primates; Catarrhin
1 (bases 1 to 526)
Dias Neto,E., Garcia Correa,R., Verjovs
Nagai,M.A., da Silva,W. Jr., Zago,M.A.,
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/db_xref="taxon:99883"
/clone="107F05"
/clone_lib="G"
/note="Genoscope sequence ID : COAG1
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Pred. No. 1.1e-31;
2; Mismatches 166;
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                                          Craniata; Vertebrata; Catarrhini; Hominidae;
   Verjovski-Almeida,S.,
go,M.A., Bordin,S., Co
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   Costa, F.F.,
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nigroviridis
                                                            Euteleostomi;
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hes 246;
                                                                                                                                            gtcttcaatccagtggaaatatgttatcaacttgtgtgggcaagattttcccctgaagtc
                                                                                                                                                                                                                                                                                                 catgaacaatttagctaagtgcttctccaatattttcattgcttccaaattagaggctgt 584
                                                                                                                                                                                                                                                                                                                                                                                                                                   CACAGTGACCATCCACAAAGACTTCGGCACTTTTGAGCGGCTCTTCAGGGCGATTTATAT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGAAGCCACTATGTAACAGAAACACTCTCTGAAGAAGAGGCTGGGTTCCCTTTAGCTTA 438
                                       CAACAGGGAAATAGTTCAGTATCTGAAGGGATTTAAAGGGAAAAATAT
                                                                         aaattttgaattggtgtcagagttgaaaaaactcaatggagcaaatat 752
                                                                                                                   CTCTGAAGTTCCCTGGAAGTATGTCATCAACACCCGGGGGCAAGACTTTCCCCTGAAAAC
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                                                                                                                                                                                                                                                                            AGTGAAACAGTTACTCAGCTGCTTCCCAAATGCTTTTCTGGCTTCCAAGAAGGAGTCGGT
                                                                                                                                                                                                                                                                                                                                                       GCCCCCAAATGTCTACTGTGCACCTGGATCAGAAGGCGACGGATGCCTTTAAAGGTGC
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High quality sequence stop: 526.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=MRO-BN0115-020

300-001-a03st3=2000-03-02st4=1)

Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G
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Ludwig Institute
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16; Conservative
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wig Institute for Cancer Research
Prof. Antonio Prudente 109, 4 andar,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: breast_normal; Vector: puc18: Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:9606"
/clone_lib="BN0115"
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Pred. No. 2.4e-29;
0; Mismatches 162;
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  CTATAAAGAGCAATGCAGAGATGGTCCAGGCTCTCAAGATGTTGAATGGGAGGAATAGCA
                                 ccctgaagtcaaattttgaattggtgtcagagttgaaaaaactcaatggagcaaatatgt 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caatagoctattotttggttgtocacaaagatgoaattatggttgaaaggcttatocatg 454
                               accttotgaagtottcaatocagtggaaatatgttatcaacttgtgtggggcaagattttc 694
                                                                                                                TGGTTCGGGTGGTTTATGCCTCCTGGTCCAGGGTGCAAGCTGACCTCAACTGCATGGAAG 240
                                                                                                                                                  CTGTGTATGCCCCTCAGAACATATACTGTGTCCATGTGGATGAGAAGTCCCCAGAAACTT
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High quality sequence stop: 606.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant);
/lab_host="DH10B (phage-resistant);
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CONA made by oligo-dT priming. Directionally
cloned into ECORI,XhoI sites using the following 5,
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
81 a 137 c 140 g 154 t
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/clone_lib="NIH_MGC_15"
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/db_xref="taxon:9606"
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Pred. No. 2.5e-29;
D; Mismatches 272;
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AZ388491
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ388491 567 bp DNA GSS 02-OCT-: 1M0148G03R Mouse 10kb plasmid UUGC1M library Mus musculus cione UUGC1M0148G03 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                            Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B.
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801 585 7177
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/SG (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/GJ"
/db_xref="haxon:10090"
/clone="UUGC1M0148G03"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Matches 275; Conservative
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acttaccatcatgaacttaga 816
                                                        TTGAAAGGGCAGAACAGTATGGAGTCAGAGGTACCACCTCCACATAAAAAATCCCGCTGG
                                                                                                      ctcaatggagcaaatatgttggagacggtgaaaccccccaaacagtaaattggaaagattc
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